

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 24, 2003, 07:22:18 ; Search time 21 Seconds
(without alignments)
2678.030 Million cell updates/sec

Title: us-09-833-111-18

Perfect score: 3103

Sequence: 1 DAHKSEVAHFKDLGEENFK.....TCFAEKGKLVAAASQAALGL 585

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3103	100.0	609	1 ABHUS	serum albumin prec
2	2942	94.8	600	2 A47391	serum albumin prec
3	2820	84.4	608	2 S7632	serum albumin prec
4	2475.5	79.8	607	1 ABHOS	serum albumin prec
5	2446.5	78.8	607	1 ABBOS	serum albumin prec
6	2432.5	78.4	607	1 ABBOS	serum albumin prec
7	2426	78.2	608	1 ABBOS	serum albumin prec
8	2411.5	77.7	605	1 ABPGS	serum albumin prec
9	2387	76.9	609	2 JC5838	albumin - Mongolia
10	1861	60.0	453	2 A05139	serum albumin - mo
11	1557.5	50.2	615	1 ABCSHS	serum albumin prec
12	1253.5	40.4	609	2 JC4258	alpha-fetoprotein
13	1249.5	40.3	609	1 FPHU	alpha-fetoprotein
14	1242.5	40.0	609	1 FPGO	alpha-fetoprotein
15	1205	38.8	607	1 ABXL72	74K albumin prec
16	1181.5	38.1	265	2 I46986	albumin - dog (ira
17	1175.5	37.9	608	1 ABXL68	68K serum albumin
18	1084	34.9	605	1 FPM5	alpha-fetoprotein
19	1067	34.4	611	1 FPRP	alpha-fetoprotein
20	1055	34.0	599	1 A34906	afamin precursor -
21	928.5	29.9	614	2 S59517	serum albumin prec
22	928	29.9	608	2 A53195	afamin precursor -
23	747.5	24.1	608	1 ABONS1	serum albumin 1 pr
24	742.5	23.9	608	1 ABONS2	serum albumin 2 pr
25	699	22.5	382	2 A37253	serum albumin - bu
26	440.5	14.2	1423	1 S27941	serum albumin - se
27	386	12.4	474	1 VYHUI	vitamin D-binding
28	385	12.4	476	1 VVRTD	vitamin D-binding
29	372	12.0	472	1 A35327	vitamin D-binding

RESULT 1

ABHUS

serum albumin precursor [validated] - human

N:Alternate names: preproalbumin

N:Contains: Kinetensin

C:Species: Homo sapiens (man)

C:Date: 29-Jul-1981 #sequence-revision 31-Jan-1997 #text-change 17-Mar-2000

C:Accession: A93743; A93936; I39427; I59286; I59313; G01747; S55314; A91420; S06422;

R:Lawn, R.M.; Adelman, J.; Bock, S.C.; Franke, A.E.; Houck, C.M.; Najarian, R.C.; Se

Nucleic Acids Res. 9, 6103-6114, 1981

A:Title: The sequence of human serum albumin cDNA and its expression in Escherichia

A:Reference number: A93743; MUID:82081882; PMID:6171778

A:Accession: A93743

A:Molecule type: mRNA

A:Residues: 1-419, K, 421-609 <LAW>

A:Cross-references: EMBL:V00495; GB:J00078; GB:L00132; GB:L00133; NID:g28591; PIDN:C

R:Dugaiczky, A.; Law, S.W.; Dennison, O.E.

Proc. Natl. Acad. Sci. U.S.A. 79, 71-75, 1982

A:Title: Nucleotide sequence and the encoded amino acids of human serum albumin mRNA

A:Reference number: A93936; MUID:82105994; PMID:6275391

A:Accession: A93936

A:Molecule type: mRNA

A:Residues: 1-120, 'G', 122-609 <DUG>

A:Cross-references: EMBL:V00494; NID:g28589; PIDN:CAA23753.1; PID:g28590

R:Urano, Y.; Watanabe, K.; Sakai, M.; Tamaoki, T.

J. Biol. Chem. 261, 3244-3251, 1986

A:Title: The human albumin gene. Characterization of the 5' and 3' flanking regions

A:Reference number: I39427; MUID:86140099; PMID:2419329

A:Accession: I39427

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-26 <ORA>

A:Cross-references: GB:M13075; NID:g178330; PIDN:AAA51688.1; PID:g553173

R:Watkins, S.; Madison, J.; Galliano, M.; Minchiotti, L.; Putnam, F.W.

Proc. Natl. Acad. Sci. U.S.A. 91, 2275-2279, 1994

A:Title: A nucleotide insertion and frameshift cause analbuminemia in an Italian fam

A:Reference number: I59286; MUID:94181575; PMID:8134387

A:Accession: I59286

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 282-290, 'KSRFDLQ' <WAT>

A:Cross-references: GB:S69192; NID:g546032; PIDN:AAB30282.1; PID:g546033

A:Note: this frame-shift variant, designated albumin Roma, leads to analbuminemia

R:Madison, J.; Galliano, M.; Watkins, S.; Minchiotti, L.; Porta, F.; Rossi, A.; Putn

Proc. Natl. Acad. Sci. U.S.A. 91, 6476-6480, 1994

A:Title: Genetic variants of human serum albumin in Italy: point mutants and a carb

A:Reference number: I59313; MUID:94294404; PMID:8022807

A:Accession: I59313

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 589-590, 'ALPRRVKNLIQVKLP' <MAD>

A:Cross-references: GB:S70799; NID:g547231; PIDN:AAB31177.1; PID:g547232

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A:Note: this frame-shift variant is designated albumin Bazzano; four additional variants submitted to the EMBL Data Library, March 1995
 A:Reference number: G08292
 A:Accession: G01747
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-120, 'G', 122-455 <MEN>
 A:Cross-references: EMBL:U22361; NID:G763428; PIDN:AAA64922.1; PID:G763431
 R:Ledgerwood, E.C.; George, P.M.; Peach, R.J.; Brennan, S.O.
 Biochem. J. 308, 321-325, 1995
 A:Title: Endoproteolytic processing of recombinant proalbumin variants by the yeast Kex2
 A:Reference number: S55314; MUID:95275251; PMID:7755581
 A:Accession: S55314
 A:Molecule type: protein
 A:Residues: 19-27 <LED>
 R:Meloun, B.; Moravsek, L.; Kostka, V.
 FEBS Lett. 58, 134-137, 1975
 A:Title: Complete amino acid sequence of human serum albumin.
 A:Reference number: A91420; MUID:76187907; PMID:1225573
 A:Accession: A91420
 A:Molecule type: protein
 A:Residues: 25-117, 'EQ', 120-154, 'Q', 156-193, 'E', 195-387, 'H', 389-390, 'Y', 392-393, 'A', 395-396, 'R', 397-400, 'D', 401-402, 'E', 403-404, 'K', 405-406, 'R', 407-408, 'E', 409-410, 'D', 411-412, 'E', 413-414, 'K', 415-416, 'R', 417-418, 'E', 419-420, 'D', 421-422, 'E', 423-424, 'K', 425-426, 'R', 427-428, 'E', 429-430, 'D', 431-432, 'E', 433-434, 'K', 435-436, 'R', 437-438, 'E', 439-440, 'D', 441-442, 'E', 443-444, 'K', 445-446, 'R', 447-448, 'E', 449-450, 'D', 451-452, 'E', 453-454, 'K', 455-456, 'R', 457-458, 'E', 459-460, 'D', 461-462, 'E', 463-464, 'K', 465-466, 'R', 467-468, 'E', 469-470, 'D', 471-472, 'E', 473-474, 'K', 475-476, 'R', 477-478, 'E', 479-480, 'D', 481-482, 'E', 483-484, 'K', 485-486, 'R', 487-488, 'E', 489-490, 'D', 491-492, 'E', 493-494, 'K', 495-496, 'R', 497-498, 'E', 499-500, 'D', 501-502, 'E', 503-504, 'K', 505-506, 'R', 507-508, 'E', 509-510, 'D', 511-512, 'E', 513-514, 'K', 515-516, 'R', 517-518, 'E', 519-520, 'D', 521-522, 'E', 523-524, 'K', 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F:166-174/Product: kinetensin #status experimental <KIP>
 F:221-394/Domain: serum albumin repeat homology <SA2>
 F:413-592/Domain: serum albumin repeat homology <SA2>
 F:27/Binding site: copper (His) #status predicted
 F:77-86.99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-385,384-393,413-592/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 100.0%; Score 3103; DB 1; Length 609;
 Best Local Similarity 100.0%; Pred. No. 7.4e-198;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHFKDLGEENFKALVLIATFAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 60
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 DB 25 DAHSEVAHFKDLGEENFKALVLIATFAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 84
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 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLPLRVREPV 120
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 DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLPLRVREPV 144
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 DB 145 DVMCTAFHDNEETFLKKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 204
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 QY 181 KLDELDEGRKASSAKORLKCAQKQGERAFKAWAVARLSORFPKAEFAEYVKLVTDLT 240
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 DB 205 KLDELDEGRKASSAKORLKCAQKQGERAFKAWAVARLSORFPKAEFAEYVKLVTDLT 264
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 QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCECKPLLEKSHCIAEVENDEMPA 300
 |||||
 DB 265 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCECKPLLEKSHCIAEVENDEMPA 324
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 QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYIYARRHPDYSVVLRLAKTYETTLK 360
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 DB 325 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYIYARRHPDYSVVLRLAKTYETTLK 384
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 QY 361 CAADPHECYAKVDFEPLVEEPQNLKQNCSELFQYKFNALLVRYTKVPQVST 420
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 DB 385 CAADPHECYAKVDFEPLVEEPQNLKQNCSELFQYKFNALLVRYTKVPQVST 444
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 QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
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 DB 445 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 504
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 QY 481 LVNRRPCFSALEVDETVVPKEFNAETTFHADICTLSEKERQIKKQATLVLYVKKHPKAT 540
 |||||
 DB 505 LVNRRPCFSALEVDETVVPKEFNAETTFHADICTLSEKERQIKKQATLVLYVKKHPKAT 564
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 QY 541 KEOLKAVMDFAAFVEKCKRADDKTCFAEEGKKLVAAASQAALGL 585
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 DB 565 KEOLKAVMDFAAFVEKCKRADDKTCFAEEGKKLVAAASQAALGL 609
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RESULT 2

A47391
 serum albumin precursor - rhesus macaque
 C:Species: Macaca mulatta (rhesus macaque)
 C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
 R:Accession: A47391
 R:Watkins, S.; Sakamoto, Y.; Madison, J.; Davis, E.; Smith, D.G.; Dwulet, J.; Putnam, F.
 Proc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993
 A:Title: cDNA and protein sequence of polymorphic macaque albumins that differ in biliru-
 A:Reference number: A47391; MUID:93211971; PMID:8460152
 A:Contents: B/B homozygote
 A:Accession: A47391
 A:Status: preliminary
 A:Molecule type: mRNA; protein
 A:Residues: 1-600 <WAT>
 A:Cross-references: GB:M90463; NID:g342294; PIDN:AAA36906.1; PID:g342295
 A:Experimental source: liver
 A:Note: sequence extracted from NCBI backbone (NCBIN:128280, NCBI:P128281)
 C:Superfamily: serum albumin; serum albumin repeat homology
 F:21-194/Domain: serum albumin repeat homology <SA1>
 F:213-386/Domain: serum albumin repeat homology <SA2>

F:405-584/Domain: serum albumin repeat homology <SA3>

Query Match 94.8%; Score 2942; DB 2; Length 600;
 Best Local Similarity 93.5%; Pred. No. 3.3e-187;
 Matches 545; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

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 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLPLRVREPV 120
 |||||
 DB 77 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLPLRVREPV 136
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 QY 121 DVMCTAFHDNEETFLKKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
 |||||
 DB 137 DVMCTAFHDNEETFLKKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 196
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 QY 181 KLDELDEGRKASSAKORLKCAQKQGERAFKAWAVARLSORFPKAEFAEYVKLVTDLT 240
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 DB 197 KLDELDEGRKASSAKORLKCAQKQGERAFKAWAVARLSORFPKAEFAEYVKLVTDLT 256
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 QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCECKPLLEKSHCIAEVENDEMPA 300
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 DB 257 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCECKPLLEKSHCIAEVENDEMPA 316
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 QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYIYARRHPDYSVVLRLAKTYETTLK 360
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 DB 317 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYIYARRHPDYSVVLRLAKTYETTLK 376
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 QY 361 CAADPHECYAKVDFEPLVEEPQNLKQNCSELFQYKFNALLVRYTKVPQVST 420
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 DB 377 CAADPHECYAKVDFEPLVEEPQNLKQNCSELFQYKFNALLVRYTKVPQVST 436
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 QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
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 DB 437 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 496
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 QY 481 LVNRRPCFSALEVDETVVPKEFNAETTFHADICTLSEKERQIKKQATLVLYVKKHPKAT 540
 |||||
 DB 497 LVNRRPCFSALEVDETVVPKEFNAETTFHADICTLSEKERQIKKQATLVLYVKKHPKAT 556
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 QY 541 KEOLKAVMDFAAFVEKCKRADDKTCFAEEGKKLVAAASQAAL 583
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 DB 557 KEOLKAVMDFAAFVEKCKRADDKTCFAEEGKKLVAAASQAAL 599
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RESULT 3

S57632
 serum albumin precursor - cat
 C:Species: Felis silvestris catus (domestic cat)
 C:Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Aug-1999
 C:Accession: JCA660; S57632
 R:Hilger, C.; Grigioni, F.; Hentges, F.
 Gene 169, 295-296, 1996
 A:Title: Sequence of the gene encoding cat (Felis domesticus) serum albumin.
 A:Reference number: JCA660; MUID:96194824; PMID:8647469
 A:Accession: JCA660
 A:Molecule type: mRNA
 A:Residues: 1-608 <HI2>
 A:Cross-references: EMBL:X84842; NID:g886484; PIDN:CAA59279.1; PID:g886485
 A:Experimental source: liver
 A:Comment: This protein is the major protein component in plasma. It functions as a p
 ein has 35 conserved cysteine residues
 C:Superfamily: serum albumin; serum albumin repeat homology
 C:Keywords: liver; plasma
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PRP>
 F:25-608/Product: serum albumin #status predicted <MAT>
 F:29-202/Domain: serum albumin repeat homology <SA1>
 F:221-394/Domain: serum albumin repeat homology <SA2>
 F:413-592/Domain: serum albumin repeat homology <SA3>

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QY 121 DVMCTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
Db 121 DVMCTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
QY 181 KLDELDEGKASSAKQRLKASQKFGKAFKAWARLSORFFKAEVSKLVTLDTK 240
Db 181 KLDELDEGKASSAKQRLKASQKFGKAFKAWARLSORFFKAEVSKLVTLDTK 240
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCECKPLLEKSHCIAEVENDEMPA 300
Db 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCECKPLLEKSHCIAEVENDEMPA 300
QY 301 DLPSSLAADFVESKDVCKNTAEAKDVLGMFLYIARRHPDYSVLLRLAKYETTLTK 360
Db 301 DLPSSLAADFVESKDVCKNTAEAKDVLGMFLYIARRHPDYSVLLRLAKYETTLTK 360
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Db 361 CAADPHCEYAKVDFEFLPVEEPQNLKQNCLEFQGEYKFNALLVRYTKKVPQVST 420
QY 421 PTLVEVSRNLGVSKCKHPEAKRMPCAEDYLSVNLQCLVLEKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRNLGVSKCKHPEAKRMPCAEDYLSVNLQCLVLEKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALEVDYTPKFEFNAETFFHADICTLSEKQIKKQATLVELVKKPKAT 540
Db 481 LVNRRPCFSALEVDYTPKFEFNAETFFHADICTLSEKQIKKQATLVELVKKPKAT 540
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Db 541 KEQLKAVMDPFAAFVEKCKRADDKTCFAEKGKLVAAQAALGL 585

W097 12-14-15

RESULT 5
AAO20111
ID AAO20111 standard; Protein; 585 AA.
XX AAO20111;
XX AAO20111;
DT 06-AUG-2002 (first entry)
DE HSA protein sequence related to the growth hormone protein.
KW Serum albumin-growth hormone fusion protein; growth hormone;
KW Down's syndrome.
OS Unidentified.
PN KR99076789-A.
PD 15-OCT-1999.
PF 25-JUN-1998; 98KR-0704914.
PR 30-DEC-1995; 95GB-0026733.
PR 19-DEC-1996; 96WO-GB03164.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
DR WPI; 1997-363680/55.
DR N-PSDB; AAK99568.
XX
PT Serum albumin-growth hormone fusion protein - useful to treat growth
PT hormone related diseases, e.g. Down's syndrome
XX Disclosure; Fig 6; 21pp; Korean.
XX The invention relates to a serum albumin-growth hormone fusion protein -
CC useful to treat growth hormone related diseases such as Down's syndrome.
CC This sequence represents a HSA protein related to the serum albumin-
CC growth hormone protein of the invention.

585 AA;

08:06

Query Match 100.0%; Score 3103; DB 18; Length 585;
Best Local Similarity 100.0%; Pred. No. 1e-254;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPNERNECFLOHKDDNPNLPLRVPEV 120
QY 121 DVMCTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
Db 121 DVMCTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
QY 181 KLDELDEGKASSAKQRLKASQKFGKAFKAWARLSORFFKAEVSKLVTLDTK 240
Db 181 KLDELDEGKASSAKQRLKASQKFGKAFKAWARLSORFFKAEVSKLVTLDTK 240
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCECKPLLEKSHCIAEVENDEMPA 300
Db 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCECKPLLEKSHCIAEVENDEMPA 300
QY 301 DLPSSLAADFVESKDVCKNTAEAKDVLGMFLYIARRHPDYSVLLRLAKYETTLTK 360
Db 301 DLPSSLAADFVESKDVCKNTAEAKDVLGMFLYIARRHPDYSVLLRLAKYETTLTK 360
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Db 361 CAADPHCEYAKVDFEFLPVEEPQNLKQNCLEFQGEYKFNALLVRYTKKVPQVST 420
QY 421 PTLVEVSRNLGVSKCKHPEAKRMPCAEDYLSVNLQCLVLEKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRNLGVSKCKHPEAKRMPCAEDYLSVNLQCLVLEKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALEVDYTPKFEFNAETFFHADICTLSEKQIKKQATLVELVKKPKAT 540
Db 481 LVNRRPCFSALEVDYTPKFEFNAETFFHADICTLSEKQIKKQATLVELVKKPKAT 540
QY 541 KEQLKAVMDPFAAFVEKCKRADDKTCFAEKGKLVAAQAALGL 585
Db 541 KEQLKAVMDPFAAFVEKCKRADDKTCFAEKGKLVAAQAALGL 585

RESULT 6
AAO20111
ID AAY84873 standard; protein; 585 AA.
XX AAY84873;
XX AAY84873;
DT 08-AUG-2000 (first entry)
DE Amino acid sequence of a human albumin protein.
XX Human; albumin; ischemic state; serum protein; metal ion salt;
KW perloperative ischemia; ischemia; myocardial infarction;
KW progressive coronary artery disease.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "optionally acetylated, and claimed under
FT claim 56"
XX
PN WO200020840-A1
XX
PD 13-APR-2000.
XX
PF 01-OCT-1999; 99WO-US22905.
XX

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; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: Region
;   LOCATION: 369..419
;   OTHER INFORMATION: /note= "Alternative C-termini of
;   OTHER INFORMATION: HSA(1-n)"
; FEATURE:
;   NAME/KEY: Region
;   LOCATION: 1..585
;   OTHER INFORMATION: /note= "Amino acid sequence of
;   OTHER INFORMATION: natural HSA"
; US-08-153-799-14

Query Match      100.0%; Score 3103; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 6.6e-287;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DAHSEVAHREKDLGEENFKALVLIATAFYAQYLOQCPFFEDHVKLVNEVTEFAKTCVADSEAE 60
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Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPMLPRLVRPEV 120
Qy 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELFFAKRYKAAFTCCQAAADKAACLLP 180
Db 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELFFAKRYKAAFTCCQAAADKAACLLP 180
Qy 181 KLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRPFAEYVKLVTDLT 240
Db 181 KLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRPFAEYVKLVTDLT 240
Qy 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKCECKEPPLLEKSHCIAEVENDEMPA 300
Db 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKCECKEPPLLEKSHCIAEVENDEMPA 300
Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVVLLRLAKTYETTLK 360
Db 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVVLLRLAKTYETTLK 360
Qy 361 CAADPHCEYAKVDFEKLVEEPQNLIKONCELFQELGKVFONALLVRYTKKVPQVST 420
Db 361 CAADPHCEYAKVDFEKLVEEPQNLIKONCELFQELGKVFONALLVRYTKKVPQVST 420
Qy 421 PTLVEVSRNLGKVGSKCKHPKAKRMPCAEYLSVWLNQLCVLHEKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRNLGKVGSKCKHPKAKRMPCAEYLSVWLNQLCVLHEKTPVSDRVTKCCTES 480
Qy 481 LVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQATLVLYVKKPKAT 540
Db 481 LVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQATLVLYVKKPKAT 540
Qy 541 KEQLKAVMDFFAAVEKCCCKADDETCTFAEGKKLVAAASQAALGL 585
Db 541 KEQLKAVMDFFAAVEKCCCKADDETCTFAEGKKLVAAASQAALGL 585

RESULT 2
US-08-702-572-2
; Sequence 2, Application US/08702572
; Patent No. 5965386
; GENERAL INFORMATION:
;   APPLICANT: Kerry-Williams, Sean M
;   APPLICANT: Gilbert, Sarah C
;   TITLE OF INVENTION: Yeast Strains and Modified Albumins
;   NUMBER OF SEQUENCES: 16
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Centeon L.L.C.
;   STREET: 1020 First Avenue
;   .. ..
```

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; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08702,572
; FILING DATE: 11-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 95/23857
; FILING DATE: 1-MAR-1995
; APPLICATION NUMBER: GB 9404270.2
; FILING DATE: 5-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Naomi Biswas
; REGISTRATION NUMBER: 38,384
; REFERENCE/DOCKET NUMBER: CE0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610/878/4294
; TELEFAX: 610/878/4221
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-572-2

Query Match      100.0%; Score 3103; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 6.6e-287;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHSEVAHREKDLGEENFKALVLIATAFYAQYLOQCPFFEDHVKLVNEVTEFAKTCVADSEAE 60
Db 1 DAHSEVAHREKDLGEENFKALVLIATAFYAQYLOQCPFFEDHVKLVNEVTEFAKTCVADSEAE 60
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPMLPRLVRPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPMLPRLVRPEV 120
Qy 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELFFAKRYKAAFTCCQAAADKAACLLP 180
Db 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELFFAKRYKAAFTCCQAAADKAACLLP 180
Qy 181 KLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRPFAEYVKLVTDLT 240
Db 181 KLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRPFAEYVKLVTDLT 240
Qy 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKCECKEPPLLEKSHCIAEVENDEMPA 300
Db 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKCECKEPPLLEKSHCIAEVENDEMPA 300
Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVVLLRLAKTYETTLK 360
Db 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVVLLRLAKTYETTLK 360
Qy 361 CAADPHCEYAKVDFEKLVEEPQNLIKONCELFQELGKVFONALLVRYTKKVPQVST 420
Db 361 CAADPHCEYAKVDFEKLVEEPQNLIKONCELFQELGKVFONALLVRYTKKVPQVST 420
Qy 421 PTLVEVSRNLGKVGSKCKHPKAKRMPCAEYLSVWLNQLCVLHEKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRNLGKVGSKCKHPKAKRMPCAEYLSVWLNQLCVLHEKTPVSDRVTKCCTES 480
Qy 481 LVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQATLVLYVKKPKAT 540
Db 481 LVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQATLVLYVKKPKAT 540
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Qy 541 KEQLKAVMDPFAAFVEKCKKADKCTFAEKGKLVAAASQAALGL 585
Db 541 KEQLKAVMDPFAAFVEKCKKADKCTFAEKGKLVAAASQAALGL 585

RESULT 3

US-08-769-746-2
: Sequence 2, Application US/08769746
: Patent No. 6274305
: GENERAL INFORMATION:
: APPLICANT: Sonnenschein, Carlos
: APPLICANT: Soto, Ana M.
: TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Medlen & Carroll, LLP
: STREET: 220 Montgomery Street, Suite 2200
: CITY: San Francisco
: STATE: California
: COUNTRY: United States of America
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/769,746
: FILING DATE: 19-DEC-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Carroll, Peter G.
: REGISTRATION NUMBER: 32,837
: REFERENCE/DOCKET NUMBER: MBRI-02584
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 705-8410
: TELEFAX: (415) 397-8338
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 585 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-769-746-2

Query Match 100.0%; Score 3103; DB 4; Length 585;
Best Local Similarity 100.0%; Pred. No. 6.6e-287;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHSEVAHREKDLGEENFKALVLIATAQYLQCCPFEDHVKLVNEVTEFAKTCVADSAE 60
Db 1 DAHSEVAHREKDLGEENFKALVLIATAQYLQCCPFEDHVKLVNEVTEFAKTCVADSAE 60
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEERNECFLOKDKDNPMLPLRVPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEERNECFLOKDKDNPMLPLRVPEV 120
Qy 121 DVMCTAFHDNEETFLKYLIEIARRHPYFYAPPELLFTAKRYKAFTCCQAADKAACLLP 180
Db 121 DVMCTAFHDNEETFLKYLIEIARRHPYFYAPPELLFTAKRYKAFTCCQAADKAACLLP 180
Qy 181 KLDELDRDGKASSAKORLKASLOKFGERAFKANAVARLSORFPKAEVSKLVTDLTK 240
Db 181 KLDELDRDGKASSAKORLKASLOKFGERAFKANAVARLSORFPKAEVSKLVTDLTK 240
Qy 241 VHTCCCHGDLLECADRADLAKYICENQDSISLKECCERPLEKSHCIAEVENDEMPA 300
Db 241 VHTCCCHGDLLECADRADLAKYICENQDSISLKECCERPLEKSHCIAEVENDEMPA 300
Qy 301 DLPSLAADFVESKDVCKNYAKADKDFVGMFLYFYARRHPDYSVVLLLRKAKTYETTLK 360
Db 301 DLPSLAADFVESKDVCKNYAKADKDFVGMFLYFYARRHPDYSVVLLLRKAKTYETTLK 360

Qy 361 CAAADPHCYAKVDFEFKPLVEEPQNLKQKONCELFQELGKEYKFQNALLVRYTKKVPQVST 420
Db 361 CAAADPHCYAKVDFEFKPLVEEPQNLKQKONCELFQELGKEYKFQNALLVRYTKKVPQVST 420
Qy 421 PTLVEVSRNLGKVGSKCKKHPKAPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRNLGKVGSKCKKHPKAPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Qy 481 LVNRRPCFSALEVDVETVYPKEFNAETFTFHADICTLSEKQRIKQTALVELVHKPKAT 540
Db 481 LVNRRPCFSALEVDVETVYPKEFNAETFTFHADICTLSEKQRIKQTALVELVHKPKAT 540
Qy 541 KEQLKAVMDPFAAFVEKCKKADKCTFAEKGKLVAAASQAALGL 585
Db 541 KEQLKAVMDPFAAFVEKCKKADKCTFAEKGKLVAAASQAALGL 585

RESULT 4

US-08-797-689-2
: Sequence 2, Application US/08797689
: Patent No. 5876969
: GENERAL INFORMATION:
: APPLICANT: Fleer, Reinhard
: APPLICANT: Fournier, Alain
: APPLICANT: Guitton, Jean-Dominique
: APPLICANT: Jung, Gerard
: APPLICANT: Yeh, Patrice
: TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
: TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Rhone-Poulenc Rorer Inc.
: STREET: 500 Arcola Road, 3C43
: CITY: Collegeville
: STATE: PA
: COUNTRY: USA
: ZIP: 19426
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Macintosh
: OPERATING SYSTEM: System 7.1
: SOFTWARE: Word 5.1 (patentin)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/797,689
: FILING DATE: 31-JAN-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/256,927
: FILING DATE: 28-JUL-1994
: APPLICATION NUMBER: FR 92/01064
: FILING DATE: 31-JAN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/FR93/00085
: FILING DATE: 28-JAN-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith Ph.D., Julie K.
: REGISTRATION NUMBER: P-38,619
: REFERENCE/DOCKET NUMBER: ST92006-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (610) 454-3839
: TELEFAX: (610) 454-3808
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 610 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-797-689-2

Query Match 100.0%; Score 3103; DB 2; Length 610;
Best Local Similarity 100.0%; Pred. No. 7e-287;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match	Best Local Similarity	Score	DB 1	Length	DB 2	Length	DB 3	Length
Query Match	Best Local Similarity	Score	DB 1	Length	DB 2	Length	DB 3	Length
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
QY 1	DAKSEVAHFRKDLGKLTCTVATLRETYGEMADCCAKOEPERNECFQHKDDNPNLRLVRPEV	100.0%;	3103;	787;				
DB 203	DAKSEVAHFRKDLGKLTCTVATLRETYGEMADCCAKOEPERNECFQHKDDNPNLRLVRPEV	100.0%;	3103;	787;				
QY 61	NDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFQHKDDNPNLRLVRPEV	100.0%;	3103;	787;				
DB 263	NDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFQHKDDNPNLRLVRPEV	100.0%;	3103;	787;				
QY 121	DVMTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQADKAACLLP	100.0%;	3103;	787;				
DB 323	DVMTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQADKAACLLP	100.0%;	3103;	787;				
QY 181	KLDELDEGKASSAKORLKASQKFGERAFAKAWARLSORFPKAEFVSKLVTDLTK	100.0%;	3103;	787;				
DB 383	KLDELDEGKASSAKORLKASQKFGERAFAKAWARLSORFPKAEFVSKLVTDLTK	100.0%;	3103;	787;				
QY 1	DAKSEVAHFRKDLGKLTCTVATLRETYGEMADCCAKOEPERNECFQHKDDNPNLRLVRPEV	100.0%;	3103;	787;				
DB 203	DAKSEVAHFRKDLGKLTCTVATLRETYGEMADCCAKOEPERNECFQHKDDNPNLRLVRPEV	100.0%;	3103;	787;				
QY 61	NDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFQHKDDNPNLRLVRPEV	100.0%;	3103;	787;				
DB 263	NDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFQHKDDNPNLRLVRPEV	100.0%;	3103;	787;				
QY 121	DVMTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQADKAACLLP	100.0%;	3103;	787;				
DB 323	DVMTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQADKAACLLP	100.0%;	3103;	787;				
QY 181	KLDELDEGKASSAKORLKASQKFGERAFAKAWARLSORFPKAEFVSKLVTDLTK	100.0%;	3103;	787;				
DB 383	KLDELDEGKASSAKORLKASQKFGERAFAKAWARLSORFPKAEFVSKLVTDLTK	100.0%;	3103;	787;				

QY 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCECKPILLESKSHCIAEVENDEMPA 300
 DB 443 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCECKPILLESKSHCIAEVENDEMPA 502
 QY 301 DPLSLAADFESKDVCKNYAEAKDVLGMLFYEARHHPDYSVLLRLAKTYETTTLEK 360
 DB 503 DPLSLAADFESKDVCKNYAEAKDVLGMLFYEARHHPDYSVLLRLAKTYETTTLEK 562
 QY 361 CAADPHCYAKYVDFEKLPLVEEPQNLKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 420
 DB 563 CAADPHCYAKYVDFEKLPLVEEPQNLKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 622
 QY 421 PTLVEVSRNLGVSKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
 DB 623 PTLVEVSRNLGVSKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 682
 QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
 DB 683 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 742
 QY 541 KEOLKAVMDDDFAAFVEKCKCKADDKTCFAEBEGKKLVAAASQAALGL 585
 DB 743 KEOLKAVMDDDFAAFVEKCKCKADDKTCFAEBEGKKLVAAASQAALGL 787

RESULT 8

US-08-222-619-3
 ; Sequence 3, Application US/08222619
 ; Patent No. 5652352
 ; GENERAL INFORMATION:
 ; APPLICANT: Lichenstein, Henri
 ; APPLICANT: Lyons, David
 ; APPLICANT: Wurfel, Mark
 ; APPLICANT: Wright, Samuel
 ; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Center, Patent Operations/RRC
 ; STREET: 1840 DeHavilland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: U.S.
 ; ZIP: 91320-1789
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/222,619
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 609 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein

US-08-222-619-3

Query Match 99.9%; Score 3099; DB 1; Length 609;
 Best Local Similarity 99.8%; Pred. No. 1.7e-286;
 Matches 584; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHRFDLGENFKALVIAFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 60
 DB 25 DAHSEVAHRFDLGENFKALVIAFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 84
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPNERCEFLQHKDDNPNLRLVPRV 120

DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPNERCEFLQHKDDNPNLRLVPRV 144
 QY 121 DVNCTAFHNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECOAADAACLLP 180
 DB 145 DVNCTAFHNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECOAADAACLLP 204
 QY 181 KLDELDEGKASSAKORLKCASLQKFGERAFAKAWAVARLSQRPKAEFAEVSCLVDTLTK 240
 DB 205 KLDELDEGKASSAKORLKCASLQKFGERAFAKAWAVARLSQRPKAEFAEVSCLVDTLTK 264
 QY 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCECKPILLESKSHCIAEVENDEMPA 300
 DB 265 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCECKPILLESKSHCIAEVENDEMPA 324
 QY 301 DPLSLAADFESKDVCKNYAEAKDVLGMLFYEARHHPDYSVLLRLAKTYETTTLEK 360
 DB 325 DPLSLAADFESKDVCKNYAEAKDVLGMLFYEARHHPDYSVLLRLAKTYETTTLEK 384
 QY 361 CAADPHCYAKYVDFEKLPLVEEPQNLKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 420
 DB 385 CAADPHCYAKYVDFEKLPLVEEPQNLKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 444
 QY 421 PTLVEVSRNLGVSKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
 DB 445 PTLVEVSRNLGVSKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 504
 QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
 DB 505 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 564
 QY 541 KEOLKAVMDDDFAAFVEKCKCKADDKTCFAEBEGKKLVAAASQAALGL 585
 DB 565 KEOLKAVMDDDFAAFVEKCKCKADDKTCFAEBEGKKLVAAASQAALGL 609

RESULT 9

US-08-433-037-4
 ; Sequence 4, Application US/08433037
 ; Patent No. 5707828
 ; GENERAL INFORMATION:
 ; APPLICANT: Sreekrishna, Kotikanyadan
 ; APPLICANT: Barr, Kathryn A.
 ; APPLICANT: Briarley, Russell A.
 ; APPLICANT: Thill, Gregory P.
 ; APPLICANT: Tschoop, Juerg F.
 ; TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 11530-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/433,037
 ; FILING DATE: 03-MAY-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Digiglio, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; REFERENCE/DOCKET NUMBER: 9108Z
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-433-037-4

Query Match 99.9%; Score 3099; DB 1: Length 609;
Best Local Similarity 99.8%; Pred. No. 1.7e-286;
Matches 584; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DAHSEVAHREFKDLGEENFKALVLIATAFYAQYLQOCPPFEDHVKLVNEVTEFAKTCVADESAAE 60
Db 25 DAHSEVAHREFKDLGEENFKALVLIATAFYAQYLQOCPPFEDHVKLVNEVTEFAKTCVADESAAE 84
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPERNECFLOHKDDNPMLPLRVREPV 120
Db 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPERNECFLOHKDDNPMLPLRVREPV 144
Qy 121 DVMCTAFHDNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
Db 145 DVMCTAFHDNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 204
Qy 181 KLDELDEGKASSAKQRLKCAASLQKFGERAFKAWAVARLSQRFPAEFAEVSCLVTDLT 240
Db 205 KLDELDEGKASSAKQRLKCAASLQKFGERAFKAWAVARLSQRFPAEFAEVSCLVTDLT 264
Qy 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLECCCKPILLESKSHCIAEVENDEMPA 300
Db 265 VHTCCGDLLECCADRADLAKYICENQDSISSKLECCCKPILLESKSHCIAEVENDEMPA 324
Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLK 360
Db 325 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLK 384
Qy 361 CAAADPHCYAKVDEKPLVEEPQNLKQNCLEFQELGKFKQNALLVRYTKVPQVST 420
Db 385 CAAADPHCYAKVDEKPLVEEPQNLKQNCLEFQELGKFKQNALLVRYTKVPQVST 444
Qy 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHKTTPVSDRVTKCCTES 480
Db 445 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHKTTPVSDRVTKCCTES 504
Qy 481 LVNRRPCFSALEVDVETVYKPEFNAETTFHADICTLSEKERQIKKQALVELVKKHKPKAT 540
Db 505 LVNRRPCFSALEVDVETVYKPEFNAETTFHADICTLSEKERQIKKQALVELVKKHKPKAT 564
Qy 541 KEQLKAVMDPFAAFVEKCKKADKTCFAEKGKLVAAASQAALGL 585
Db 565 KEQLKAVMDPFAAFVEKCKKADKTCFAEKGKLVAAASQAALGL 609

RESULT 10
US-08-897-956A-2
; Sequence 2, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-08-897-956A-2

Query Match 99.9%; Score 3099; DB 4: Length 609;
Best Local Similarity 99.8%; Pred. No. 1.7e-286;
Matches 584; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAHSEVAHREFKDLGEENFKALVLIATAFYAQYLQOCPPFEDHVKLVNEVTEFAKTCVADESAAE 60
Db 25 DAHSEVAHREFKDLGEENFKALVLIATAFYAQYLQOCPPFEDHVKLVNEVTEFAKTCVADESAAE 84
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPERNECFLOHKDDNPMLPLRVREPV 120
Db 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPERNECFLOHKDDNPMLPLRVREPV 144
Qy 121 DVMCTAFHDNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
Db 145 DVMCTAFHDNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 204
Qy 181 KLDELDEGKASSAKQRLKCAASLQKFGERAFKAWAVARLSQRFPAEFAEVSCLVTDLT 240
Db 205 KLDELDEGKASSAKQRLKCAASLQKFGERAFKAWAVARLSQRFPAEFAEVSCLVTDLT 264
Qy 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLECCCKPILLESKSHCIAEVENDEMPA 300
Db 265 VHTCCGDLLECCADRADLAKYICENQDSISSKLECCCKPILLESKSHCIAEVENDEMPA 324
Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLK 360
Db 325 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLK 384
Qy 361 CAAADPHCYAKVDEKPLVEEPQNLKQNCLEFQELGKFKQNALLVRYTKVPQVST 420
Db 385 CAAADPHCYAKVDEKPLVEEPQNLKQNCLEFQELGKFKQNALLVRYTKVPQVST 444
Qy 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHKTTPVSDRVTKCCTES 480
Db 445 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHKTTPVSDRVTKCCTES 504
Qy 481 LVNRRPCFSALEVDVETVYKPEFNAETTFHADICTLSEKERQIKKQALVELVKKHKPKAT 540
Db 505 LVNRRPCFSALEVDVETVYKPEFNAETTFHADICTLSEKERQIKKQALVELVKKHKPKAT 564
Qy 541 KEQLKAVMDPFAAFVEKCKKADKTCFAEKGKLVAAASQAALGL 585
Db 565 KEQLKAVMDPFAAFVEKCKKADKTCFAEKGKLVAAASQAALGL 609

RESULT 11
PCT-US95-04075-3
; Sequence 3, Application PC/TUS9504075
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRR
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04075
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids

; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 PCT-US95-04075-3

Query Match 99.9%; Score 3099; DB 5; Length 609;
 Best Local Similarity 99.8%; Pred. No. 1.7e-286;
 Matches 584; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	DAHKSEVAHFRKDLGGENFKALVLI	IAFAQYLOQC	PFEDHVKLVNEVTEFAKTCVADES	AE 60
DB	25	DAHKSEVAHFRKDLGGENFKALVLI	IAFAQYLOQC	PFEDHVKLVNEVTEFAKTCVADES	AE 84
QY	61	NCDKSLHTLFGDKLCTVATLRETY	GENADCCAKOE	PERNECFLOHKDDNPNLRLVRPEV	120
DB	85	NCDKSLHTLFGDKLCTVATLRETY	GENADCCAKOE	PERNECFLOHKDDNPNLRLVRPEV	144
QY	121	DVMCTAFHDNEETFLKKYLYEIA	RRHPYFYAP	PELLFFAKRYKAAFTCCQAAADKAACLLP	180
DB	145	DVMCTAFHDNEETFLKKYLYEIA	RRHPYFYAP	PELLFFAKRYKAAFTCCQAAADKAACLLP	204
QY	181	KLDELDEGKASSAKORLKCASLO	KGERAFKAWA	VARLSQRPKAEFAEVS	KLVTDLTK 240
DB	205	KLDELDEGKASSAKORLKCASLO	KGERAFKAWA	VARLSQRPKAEFAEVS	KLVTDLTK 264
QY	241	VHTECCHGDLLECADRADLAKYI	CENQDSISSK	LKECCCKP	LLEKSHCIAEVENDEMPA 300
DB	265	VHTECCHGDLLECADRADLAKYI	CENQDSISSK	LKECCCKP	LLEKSHCIAEVENDEMPA 324
QY	301	DLPSLAADFVSEKDVCKNYAEAK	DVFLGMFLY	EYARRHPDYSV	VLLRLAKTYETTLEK 360
DB	325	DLPSLAADFVSEKDVCKNYAEAK	DVFLGMFLY	EYARRHPDYSV	VLLRLAKTYETTLEK 384
QY	361	CAAADPHECYAKVDFEKP	LVPEPQNL	IKQNCFLFQ	LGKYEYKFNALLVRYTKKVPQVST 420
DB	385	CAAADPHECYAKVDFEKP	LVPEPQNL	IKQNCFLFQ	LGKYEYKFNALLVRYTKKVPQVST 444
QY	421	PTLVEVSRNLGVSKCCCKHPEAK	RMPCAEDYLS	VVLNQLCVLH	EKTPVSDRVTCKCTES 480
DB	445	PTLVEVSRNLGVSKCCCKHPEAK	RMPCAEDYLS	VVLNQLCVLH	EKTPVSDRVTCKCTES 504
QY	481	LVNRRFCFSALEVDETYVPKEF	NAETTFHADI	CTLSEKERQIK	KQTALVELVKKHKPKAT 540
DB	505	LVNRRFCFSALEVDETYVPKEF	NAETTFHADI	CTLSEKERQIK	KQTALVELVKKHKPKAT 564
QY	541	KEQLKAVMDFFAAFEVKCKKAD	KETCFABEG	KKLVAASQAALGL	585
DB	565	KEQLKAVMDFFAAFEVKCKKAD	KETCFABEG	KKLVAASQAALGL	609

RESULT 12
 US-08-897-956A-3
 ; Sequence 3, Application US/08897956A
 ; Patent No. 6423512
 ; GENERAL INFORMATION:
 ; APPLICANT: Mary Ellen Digan
 ; APPLICANT: Philip Lake
 ; APPLICANT: Hermann Gram
 ; TITLE OF INVENTION: Fusion Polypeptides
 ; FILE REFERENCE: 600-7244/CPA
 ; CURRENT APPLICATION NUMBER: US/08/897,956A
 ; CURRENT FILING DATE: 1997-07-21
 ; PRIOR FILING DATE: 60/022,689
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 978
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fusion polypeptide

US-08-897-956A-3

Query Match 99.7%; Score 3095; DB 4; Length 978;
 Best Local Similarity 99.8%; Pred. No. 8.1e-286;
 Matches 583; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	DAHKSEVAHFRKDLGGENFKALVLI	IAFAQYLOQC	PFEDHVKLVNEVTEFAKTCVADES	AE 60
DB	212	DAHKSEVAHFRKDLGGENFKALVLI	IAFAQYLOQC	PFEDHVKLVNEVTEFAKTCVADES	AE 271
QY	61	NCDKSLHTLFGDKLCTVATLRETY	GENADCCAKOE	PERNECFLOHKDDNPNLRLVRPEV	120
DB	272	NCDKSLHTLFGDKLCTVATLRETY	GENADCCAKOE	PERNECFLOHKDDNPNLRLVRPEV	331
QY	121	DVMCTAFHDNEETFLKKYLYEIA	RRHPYFYAP	PELLFFAKRYKAAFTCCQAAADKAACLLP	180
DB	332	DVMCTAFHDNEETFLKKYLYEIA	RRHPYFYAP	PELLFFAKRYKAAFTCCQAAADKAACLLP	391
QY	181	KLDELDEGKASSAKORLKCASLO	KGERAFKAWA	VARLSQRPKAEFAEVS	KLVTDLTK 240
DB	392	KLDELDEGKASSAKORLKCASLO	KGERAFKAWA	VARLSQRPKAEFAEVS	KLVTDLTK 451
QY	241	VHTECCHGDLLECADRADLAKYI	CENQDSISSK	LKECCCKP	LLEKSHCIAEVENDEMPA 300
DB	452	VHTECCHGDLLECADRADLAKYI	CENQDSISSK	LKECCCKP	LLEKSHCIAEVENDEMPA 511
QY	301	DLPSLAADFVSEKDVCKNYAEAK	DVFLGMFLY	EYARRHPDYSV	VLLRLAKTYETTLEK 360
DB	512	DLPSLAADFVSEKDVCKNYAEAK	DVFLGMFLY	EYARRHPDYSV	VLLRLAKTYETTLEK 571
QY	361	CAAADPHECYAKVDFEKP	LVPEPQNL	IKQNCFLFQ	LGKYEYKFNALLVRYTKKVPQVST 420
DB	572	CAAADPHECYAKVDFEKP	LVPEPQNL	IKQNCFLFQ	LGKYEYKFNALLVRYTKKVPQVST 631
QY	421	PTLVEVSRNLGVSKCCCKHPEAK	RMPCAEDYLS	VVLNQLCVLH	EKTPVSDRVTCKCTES 480
DB	632	PTLVEVSRNLGVSKCCCKHPEAK	RMPCAEDYLS	VVLNQLCVLH	EKTPVSDRVTCKCTES 691
QY	481	LVNRRFCFSALEVDETYVPKEF	NAETTFHADI	CTLSEKERQIK	KQTALVELVKKHKPKAT 540
DB	692	LVNRRFCFSALEVDETYVPKEF	NAETTFHADI	CTLSEKERQIK	KQTALVELVKKHKPKAT 751
QY	541	KEQLKAVMDFFAAFEVKCKKAD	KETCFABEG	KKLVAASQAALGL	584
DB	752	KEQLKAVMDFFAAFEVKCKKAD	KETCFABEG	KKLVAASQAALGL	795

RESULT 13
 US-08-448-196A-3
 ; Sequence 3, Application US/08448196A
 ; Patent No. 5780594
 ; GENERAL INFORMATION:
 ; APPLICANT: CARTER, DANIEL C.
 ; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
 ; TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
 ; TITLE OF INVENTION: RELATED PROTEINS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NASA
 ; STREET: MARSHALL SPACE FLIGHT CENTER
 ; CITY: HUNTSVILLE
 ; STATE: ALABAMA
 ; COUNTRY: USA
 ; ZIP: 35812
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/448,196A
 ; FILING DATE: 23-MAY-1995
 ; CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: BROAD JR., ROBERT L.
REGISTRATION NUMBER: 18,757
REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 205-544-0021
TELEFAX: 205-544-0258
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-448-196A-3

Query Match 99.7%; Score 3093; DB 1; Length 585;
Best Local Similarity 99.7%; Pred. No. 5.9e-286;
Matches 583; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVLIATAFYLOQCPEFHVHKLNVNEVTEFAKTCVADESAAE 60
Db 1 DAHKSEVAHRFKDLGEENFKALVLIATAFYLOQCPEFHVHKLNVNEVTEFAKTCVADESAAE 60

Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVPRPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVPRPEV 120

Qy 121 DVNCTAFHDNEETFLKYLIEYIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
Db 121 DVNCTAFHDNEETFLKYLIEYIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180

Qy 181 KLDELDEGKASSAKORLKCSLQKGFGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 240
Db 181 KLDELDEGKASSAKORLKCSLQKGFGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 240

Qy 241 VHTCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
Db 241 VHTCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300

Qy 301 DLPSLAADVESKDYCKNYAEAKDVFLGMFLYIYARRHPDYSVVLLRLAKTYETTLK 360
Db 301 DLPSLAADVESKDYCKNYAEAKDVFLGMFLYIYARRHPDYSVVLLRLAKTYETTLK 360

Qy 361 CAADPHCEYAKVDFEPLVEEPONLIKQNCLEFQKLGKYEYFQNALVRYTKVPQVST 420
Db 361 CAADPHCEYAKVDFEPLVEEPONLIKQNCLEFQKLGKYEYFQNALVRYTKVPQVST 420

Qy 421 PTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480

Qy 481 LVNRRPCFSALEVDYTYVPKEFNAETFTFHADICTLSEKEROIKKQATALVELVKKPKAT 540
Db 481 LVNRRPCFSALEVDYTYVPKEFNAETFTFHADICTLSEKEROIKKQATALVELVKKPKAT 540

Qy 541 KQQLKAVMDPFAAFVEKCKCKADKCTCFABEGKKLVAASQAALGL 585
Db 541 KQQLKAVMDPFAAFVEKCKCKADKCTCFABEGKKLVAASQAALGL 585

RESULT 14
US-08-984-176-1
Sequence 1, Application US/08984176
Patent No. 5948609
GENERAL INFORMATION:
APPLICANT: CARTER, DANIEL C
APPLICANT: HO, JOSEPH X
TITLE OF INVENTION: OXYGEN-TRANSPORTING ALBUMIN-BASED BLOOD REPLACEMENT
TITLE OF INVENTION: COMPOSITION AND BLOOD VOLUME EXPANDER

FILE REFERENCE: 08/984,176
CURRENT APPLICATION NUMBER: US/08/984,176
CURRENT FILING DATE: 1997-12-03
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 585
TYPE: PRT
ORGANISM: Homo sapiens
US-08-984-176-1

Query Match 99.7%; Score 3093; DB 2; Length 585;
Best Local Similarity 99.7%; Pred. No. 5.9e-286;
Matches 583; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVLIATAFYLOQCPEFHVHKLNVNEVTEFAKTCVADESAAE 60
Db 1 DAHKSEVAHRFKDLGEENFKALVLIATAFYLOQCPEFHVHKLNVNEVTEFAKTCVADESAAE 60

Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVPRPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVPRPEV 120

Qy 121 DVNCTAFHDNEETFLKYLIEYIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
Db 121 DVNCTAFHDNEETFLKYLIEYIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180

Qy 181 KLDELDEGKASSAKORLKCSLQKGFGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 240
Db 181 KLDELDEGKASSAKORLKCSLQKGFGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 240

Qy 241 VHTCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
Db 241 VHTCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300

Qy 301 DLPSLAADVESKDYCKNYAEAKDVFLGMFLYIYARRHPDYSVVLLRLAKTYETTLK 360
Db 301 DLPSLAADVESKDYCKNYAEAKDVFLGMFLYIYARRHPDYSVVLLRLAKTYETTLK 360

Qy 361 CAADPHCEYAKVDFEPLVEEPONLIKQNCLEFQKLGKYEYFQNALVRYTKVPQVST 420
Db 361 CAADPHCEYAKVDFEPLVEEPONLIKQNCLEFQKLGKYEYFQNALVRYTKVPQVST 420

Qy 421 PTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480

Qy 481 LVNRRPCFSALEVDYTYVPKEFNAETFTFHADICTLSEKEROIKKQATALVELVKKPKAT 540
Db 481 LVNRRPCFSALEVDYTYVPKEFNAETFTFHADICTLSEKEROIKKQATALVELVKKPKAT 540

Qy 541 KQQLKAVMDPFAAFVEKCKCKADKCTCFABEGKKLVAASQAALGL 585
Db 541 KQQLKAVMDPFAAFVEKCKCKADKCTCFABEGKKLVAASQAALGL 585

RESULT 15
US-08-448-196A-5
Sequence 5, Application US/08448196A
Patent No. 5780594
GENERAL INFORMATION:
APPLICANT: CARTER, DANIEL C.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
TITLE OF INVENTION: RELATED PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NASA
STREET: MARSHALL SPACE FLIGHT CENTER
CITY: HUNTSVILLE
STATE: ALABAMA
COUNTRY: USA
ZIP: 35812

Job time : 35 secs

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,196A
FILING DATE: 23-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BROAD JR., ROBERT L.
REGISTRATION NUMBER: 18,757
REFERENCE/DOCKET NUMBER: XX/WFS-28402-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 205-544-0021
TELEFAX: 205-544-0258
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-448-196A-5

Query Match 79.2%; Score 2458.5; DB 1; Length 583;
Best Local Similarity 75.8%; Pred. No. 1.5e-225;
Matches 442; Conservative 70; Mismatches 70; Indels 1; Gaps 1;

QY 1 DAHSEVAHREKDLGEENFKALVLIATAFYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 60
Db 1 DTHSETAHRENDLGEKHFGLVAVFSQYLOQCFFEDHVKLVNEVTEFAKCAADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 119
QY 121 DVMCTAFHNEETFLKYLVEIARRHRYFYAPPELLFFAKRYKAAFTCCQADKAACLLP 180
Db 120 DAQCAAFQEDDFKGLYLYEVARRHRYFYGPPELLFHAEEYKADFTECCPADDKLACLIP 179
QY 181 KLDELREGKASSAKQRLKASLQKGERAFKANAVARLSQRPFPKAEFVSKLVDTLTK 240
Db 180 KLDALKERILLSSAKERLKCSSFQNGERAVKANVARLSQKFPKADFAEVSKIIVDTLTK 239
QY 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLECCCKPLLEKSHCIAEVNDEMPPA 300
Db 240 VHKCCCHGDLLECADRADLAKYICENQDSISSKLECCCKPLLEKSHCIAEVNDEMPPA 299
QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEVARRHPDYSVVLLRLAKTYETTTLEK 360
Db 300 DIPALAADFADFEDKEICKHYKDAKDVFGLTFLYESSRHPDYSVSLLRIARTYETATLEK 359
QY 361 CAAADPHCEKAKVFEKPLVEEPONLIKONCELFGEYKFNALLVRYTKKVPQVST 420
Db 360 CAEADPPACVETVDFQTPLVVEEPKSLVKNCDLFEVGEYDFONALIVRYTKKAPQVST 419
QY 421 PTLVEVRNLGKVGSKCKHPEAKRMPCAEDYLSWLNQLCVLHEKTPVSDRVTKCCTES 480
Db 420 PTLVEIGRTLKGVSRCCKLPESERLPCSENHLALNRLCVLHEKTPVSEKITKCTDS 479
QY 481 LVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQALVELVKKHKPKAT 540
Db 480 LAERPCFSALELDEGYPVKEFAETTFHADICTLPEDEKQIKKQALVELVKKHKPKAT 539
QY 541 KEOLKAVNDFFAFAVEKCKADDKCTCFABEGKKLVAAQAAAL 583
Db 540 KEQLKTVLGNFSAFAVAKCCGREDKEACFAEGPKLVASSQAL 582
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OM protein - protein search, using sw model

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues
Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries

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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	3103	100.0	585	12 US-10-153-064-5	Sequence 5, Appli
3	3103	100.0	609	12 US-10-153-064-7	Sequence 7, Appli
4	3103	100.0	610	9 US-10-237-667-2	Sequence 2, Appli
5	3103	100.0	610	9 US-10-237-708-2	Sequence 2, Appli
6	3103	100.0	610	9 US-10-237-866-2	Sequence 2, Appli
7	3103	100.0	610	9 US-10-237-871-2	Sequence 2, Appli
8	3103	100.0	610	10 US-09-984-186-2	Sequence 2, Appli
9	3103	100.0	651	12 US-10-153-064-133	Sequence 133, App
10	3103	100.0	652	12 US-10-153-064-132	Sequence 132, App
11	3103	100.0	653	12 US-10-153-064-131	Sequence 131, App
12	3103	100.0	656	12 US-10-153-064-130	Sequence 130, App
13	3103	100.0	676	12 US-10-153-064-129	Sequence 129, App
14	3103	100.0	676	12 US-10-153-064-127	Sequence 127, App
15	3103	100.0	677	12 US-10-153-064-125	Sequence 125, App
16	3103	100.0	680	12 US-10-153-064-123	Sequence 123, App
17	3103	100.0	787	9 US-10-237-667-16	Sequence 16, Appl
18	3103	100.0	787	9 US-10-237-708-16	Sequence 16, Appl
19	3103	100.0	787	9 US-10-237-866-16	Sequence 16, Appl

20	3103	100.0	787	9 US-10-237-871-16	Sequence 16, Appl
21	3103	100.0	787	10 US-09-984-186-16	Sequence 16, Appl
22	3103	100.0	788	9 US-10-073-118-26	Sequence 26, Appl
23	3092.5	99.7	652	12 US-10-153-064-96	Sequence 96, Appl
24	3092.5	99.7	652	12 US-10-133-064-99	Sequence 99, Appl
25	3092.5	99.7	652	12 US-10-153-064-105	Sequence 105, App
26	3092.5	99.7	660	12 US-10-153-064-90	Sequence 90, Appl
27	3092.5	99.7	660	12 US-10-153-064-93	Sequence 93, Appl
28	3092.5	99.7	676	12 US-10-153-064-95	Sequence 95, Appl
29	3092.5	99.7	676	12 US-10-153-064-98	Sequence 98, Appl
30	3092.5	99.7	676	12 US-10-133-064-104	Sequence 104, App
31	3092.5	99.7	684	12 US-10-153-064-92	Sequence 92, Appl
32	3092.5	99.7	1184	12 US-10-153-064-89	Sequence 89, Appl
33	3086.5	99.5	668	12 US-10-153-064-102	Sequence 102, App
34	3086.5	99.5	692	12 US-10-153-064-101	Sequence 101, App
35	2426	78.2	608	9 US-10-165-603-24	Sequence 24, Appl
36	2426	78.2	608	9 US-10-165-603-25	Sequence 25, Appl
37	2388.5	77.0	604	9 US-10-045-170A-1	Sequence 1, Appli
38	1249.5	40.3	609	10 US-09-373-913-2	Sequence 2, Appli
39	1206.5	38.9	590	9 US-10-115-701A-2	Sequence 2, Appli
40	1206.5	38.9	590	9 US-09-940-308-2	Sequence 2, Appli
41	1048	33.8	195	9 US-10-074-956-24	Sequence 24, Appl
42	1048	33.8	241	9 US-10-074-956-27	Sequence 27, Appl
43	1048	33.8	268	9 US-10-074-956-28	Sequence 28, Appl
44	926	29.8	393	9 US-10-115-701A-7	Sequence 7, Appli
45	926	29.8	393	9 US-09-940-308-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-929-552-2
; Sequence 2, Application US/09929552
; Patent No. US20020123080A1
; GENERAL INFORMATION:
; APPLICANT: Sonnenschein, Carlos

; Soto, Ana M.

; TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medlen & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/929,552

; FILING DATE: 14-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/769,746

; FILING DATE: 19-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Carroll, Peter G.

; REGISTRATION NUMBER: 32,837

; REFERENCE/DOCKET NUMBER: MBRI-02584

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 705-8410

; TELEFAX: (415) 397-8338

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 585 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-929-552-2

Query Match 100.0%; Score 3103; DB 10; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DAHSEVAHRFKDGLGEENFKALVLIAPFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 60
DB 1 DAHSEVAHRFKDGLGEENFKALVLIAPFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
QY 121 DVMTAFHDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAACLLP 180
DB 121 DVMTAFHDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAACLLP 180
QY 181 KLDELDRDEGKASSAKQRLKCSLQKFGERAFKAWAVARLSQRPFKAEFAEVS KLVTDLTK 240
DB 181 KLDELDRDEGKASSAKQRLKCSLQKFGERAFKAWAVARLSQRPFKAEFAEVS KLVTDLTK 240
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCCCKPLLEKSHCIAEVENDEMPA 300
DB 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCCCKPLLEKSHCIAEVENDEMPA 300
QY 301 DLPDLAADFVSKDVCKNYAEAKDVFLGMFLYEVARRHPDY SVVLLRLAKTYETTLEKC 360
DB 301 DLPDLAADFVSKDVCKNYAEAKDVFLGMFLYEVARRHPDY SVVLLRLAKTYETTLEKC 360
QY 361 CAADPHCEYAKVDFEKPVLVEEPQNLIKONCELFEOQGEYKFNALLVRYTKKVPQVST 420
DB 361 CAADPHCEYAKVDFEKPVLVEEPQNLIKONCELFEOQGEYKFNALLVRYTKKVPQVST 420
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEKTPVSDRVTKKCTES 480
DB 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEKTPVSDRVTKKCTES 480
QY 481 LVNRRPCFSALEVDYTVVPKEFNAETFFHADICTLSEKERQIKKQATLVELVKKHKPKAT 540
DB 481 LVNRRPCFSALEVDYTVVPKEFNAETFFHADICTLSEKERQIKKQATLVELVKKHKPKAT 540
QY 541 KEQLKAVMDDDFAAFVEKCKCKADDDKTCFABEGKKLVAASQAALGL 585
DB 541 KEQLKAVMDDDFAAFVEKCKCKADDDKTCFABEGKKLVAASQAALGL 585
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RESULT 2
US-10-153-064-5
; Sequence 5, Application US/10153064
; Patent No. US20020142814A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-153-064-5

Query Match 100.0%; Score 3103; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DAHSEVAHRFKDGLGEENFKALVLIAPFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 60
DB 1 DAHSEVAHRFKDGLGEENFKALVLIAPFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 60
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DB 1 DAHSEVAHRFKDGLGEENFKALVLIAPFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
QY 121 DVMTAFHDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAACLLP 180
DB 121 DVMTAFHDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAACLLP 180
QY 181 KLDELDRDEGKASSAKQRLKCSLQKFGERAFKAWAVARLSQRPFKAEFAEVS KLVTDLTK 240
DB 181 KLDELDRDEGKASSAKQRLKCSLQKFGERAFKAWAVARLSQRPFKAEFAEVS KLVTDLTK 240
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCCCKPLLEKSHCIAEVENDEMPA 300
DB 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCCCKPLLEKSHCIAEVENDEMPA 300
QY 301 DLPDLAADFVSKDVCKNYAEAKDVFLGMFLYEVARRHPDY SVVLLRLAKTYETTLEKC 360
DB 301 DLPDLAADFVSKDVCKNYAEAKDVFLGMFLYEVARRHPDY SVVLLRLAKTYETTLEKC 360
QY 361 CAADPHCEYAKVDFEKPVLVEEPQNLIKONCELFEOQGEYKFNALLVRYTKKVPQVST 420
DB 361 CAADPHCEYAKVDFEKPVLVEEPQNLIKONCELFEOQGEYKFNALLVRYTKKVPQVST 420
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DB 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEKTPVSDRVTKKCTES 480
QY 481 LVNRRPCFSALEVDYTVVPKEFNAETFFHADICTLSEKERQIKKQATLVELVKKHKPKAT 540
DB 481 LVNRRPCFSALEVDYTVVPKEFNAETFFHADICTLSEKERQIKKQATLVELVKKHKPKAT 540
QY 541 KEQLKAVMDDDFAAFVEKCKCKADDDKTCFABEGKKLVAASQAALGL 585
DB 541 KEQLKAVMDDDFAAFVEKCKCKADDDKTCFABEGKKLVAASQAALGL 585
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RESULT 3

US-10-153-064-7

; Sequence 7, Application US/10153064
; Patent No. US20020142814A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-153-064-7

Query Match 100.0%; Score 3103; DB 12; Length 609;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DAHSEVAHRFKDGLGEENFKALVLIAPFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 60
DB 25 DAHSEVAHRFKDGLGEENFKALVLIAPFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 144
QY 121 DVMTAFHDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAACLLP 180
DB 121 DVMTAFHDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAACLLP 180
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Db 145 DVNCTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 204
QY 181 KLDELDECKASSAKORLKCASLQKFGERAFAKAWARLSQRFPFAEFAEVSCLVTDLTk 240
Db 205 KLDELDECKASSAKORLKCASLQKFGERAFAKAWARLSQRFPFAEFAEVSCLVTDLTk 264
QY 241 VITECHGDLLECCADRADLAKYICENQDSISSKLECECEKPLLEKSHCIAEVENDEMPA 300
Db 265 VITECHGDLLECCADRADLAKYICENQDSISSKLECECEKPLLEKSHCIAEVENDEMPA 324
QY 301 DLPSLAADPESKDVCKNYAEAKDVLGMFLYFYARRHPDYSVLLRLRAKTYETTLK 360
Db 325 DLPSLAADPESKDVCKNYAEAKDVLGMFLYFYARRHPDYSVLLRLRAKTYETTLK 384
QY 361 CAADPHCEYAKVDFEPLVEEPONLIKONCELFQGLGEYFQNALVRYTKVPQVST 420
Db 385 CAADPHCEYAKVDFEPLVEEPONLIKONCELFQGLGEYFQNALVRYTKVPQVST 444
QY 421 PTLVEVSRNLGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 445 PTLVEVSRNLGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 504
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Db 505 LVNRRPCFSALEVDYTPVKEFNAETFTPHADICTLSEKEROIKKQATALVELVKKPKAT 564
QY 541 KEQLKAVMDDDFAAFVEKCKKADDKETCFAEEGKKLVAAASQAALGL 585
Db 565 KEQLKAVMDDDFAAFVEKCKKADDKETCFAEEGKKLVAAASQAALGL 609

RESULT 4

US-10-237-667-2
; Sequence 2, Application US/10237667
; Publication No. US2003002308A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,667
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619

; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-237-667-2

Query Match 100.0%; Score 3103; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.2e-232; Indels 0; Gaps 0;
Matches 585; Conservative 0; Mismatches 0;
QY 1 DAHKSEVAHRKDLGSENFKALVLIATAFYAQYLOQCPPEHDHVKLVNEVTEFAKTCVADESAE 60
Db 25 DAHKSEVAHRKDLGSENFKALVLIATAFYAQYLOQCPPEHDHVKLVNEVTEFAKTCVADESAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
Db 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 144
QY 121 DVNCTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
Db 145 DVNCTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 204
QY 181 KLDELDECKASSAKORLKCASLQKFGERAFAKAWARLSQRFPFAEFAEVSCLVTDLTk 240
Db 205 KLDELDECKASSAKORLKCASLQKFGERAFAKAWARLSQRFPFAEFAEVSCLVTDLTk 264
QY 241 VITECHGDLLECCADRADLAKYICENQDSISSKLECECEKPLLEKSHCIAEVENDEMPA 300
Db 265 VITECHGDLLECCADRADLAKYICENQDSISSKLECECEKPLLEKSHCIAEVENDEMPA 324
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Db 325 DLPSLAADPESKDVCKNYAEAKDVLGMFLYFYARRHPDYSVLLRLRAKTYETTLK 384
QY 361 CAADPHCEYAKVDFEPLVEEPONLIKONCELFQGLGEYFQNALVRYTKVPQVST 420
Db 385 CAADPHCEYAKVDFEPLVEEPONLIKONCELFQGLGEYFQNALVRYTKVPQVST 444
QY 421 PTLVEVSRNLGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 445 PTLVEVSRNLGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 504
QY 481 LVNRRPCFSALEVDYTPVKEFNAETFTPHADICTLSEKEROIKKQATALVELVKKPKAT 540
Db 505 LVNRRPCFSALEVDYTPVKEFNAETFTPHADICTLSEKEROIKKQATALVELVKKPKAT 564
QY 541 KEQLKAVMDDDFAAFVEKCKKADDKETCFAEEGKKLVAAASQAALGL 585
Db 565 KEQLKAVMDDDFAAFVEKCKKADDKETCFAEEGKKLVAAASQAALGL 609

RESULT 5

US-10-237-708-2
; Sequence 2, Application US/10237708
; Publication No. US20030036170A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,708
FILING DATE: 10-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-237-708-2

Query Match 100.0%; Score 3103; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHFKDLGENFKALVIAFAOYLQOCPEHDHVKLVNTEFAKTCVADESAE 60
DB 25 DAHSEVAHFKDLGENFKALVIAFAOYLQOCPEHDHVKLVNTEFAKTCVADESAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 144
QY 121 DVNCTAFHDNEETFLKLYEIAARRHPYFYAPPELLFFAKRYKAFTCCOAAADKAACLLP 180
DB 145 DVNCTAFHDNEETFLKLYEIAARRHPYFYAPPELLFFAKRYKAFTCCOAAADKAACLLP 204
QY 181 KLDELDEGKASAKQRLKASLOKGERAFKAWAVARLSORPKAEFVSKLVTDLT 240
DB 205 KLDELDEGKASAKQRLKASLOKGERAFKAWAVARLSORPKAEFVSKLVTDLT 264
QY 241 VHTCCGDLLECDRADLAKYICENQDSISSKLEKCECKPLEKSHCIAEVENDEMPA 300
DB 265 VHTCCGDLLECDRADLAKYICENQDSISSKLEKCECKPLEKSHCIAEVENDEMPA 324
QY 301 DLPSLAADFVSKDVCKNYAEAKDVLGMLFYEARHPDYSVVLLRLAKTYETLEK 360
DB 325 DLPSLAADFVSKDVCKNYAEAKDVLGMLFYEARHPDYSVVLLRLAKTYETLEK 384
QY 361 CAAADPHCEYAKVDFDEKPLVEEPQNLKQNCSELFQOLGEYKFNALLVRYTKKVPQVST 420
DB 385 CAAADPHCEYAKVDFDEKPLVEEPQNLKQNCSELFQOLGEYKFNALLVRYTKKVPQVST 444
QY 421 PTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCTES 480

DB 445 PTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCTES 504
QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
DB 505 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 564
QY 541 KEQLKAVMDDDFAAFVEKCKCKADDDKCTCFABEGKKLVAAASQAALGL 585
DB 565 KEQLKAVMDDDFAAFVEKCKCKADDDKCTCFABEGKKLVAAASQAALGL 609

RESULT 6
US-10-237-866-2
; Sequence 2, Application US/10237866
; Publication No. US20030036171A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,866
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-237-866-2

Query Match 100.0%; Score 3103; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHFKDLGENFKALVIAFAOYLQOCPEHDHVKLVNTEFAKTCVADESAE 60

104 DAHSEVAHREKDLGEENFKALVLIATFAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 84
105 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 120
106 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 144
107 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 180
108 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 204
109 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 240
110 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 264
111 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 300
112 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 324
113 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 360
114 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 384
115 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 420
116 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 444
117 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 480
118 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 504
119 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 540
120 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 564

RESULT 7

US-10-237-871-2
; Sequence 2, Application US/10237871
; Publication No. US2003036172A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guillon, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (patentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,871
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927

104 DAHSEVAHREKDLGEENFKALVLIATFAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 84
105 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 120
106 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 144
107 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 180
108 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 204
109 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 240
110 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 264
111 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 300
112 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 324
113 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 360
114 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 384
115 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 420
116 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 444
117 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 480
118 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 504
119 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 540
120 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVREPV 564

RESULT 8

US-09-984-186-2
; Sequence 2, Application US/09984186
; Patent No. US2002015011A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain

Guillon, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEROF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-Oct-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-984-186-2

Query Match 100.0%; Score 3103; DB 10; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAHSEVAHFRKDLGENFKALVLIIFAQYLOQCPEDHVKLVNVEYTEFAKTCVADESAE 60
DB 25 DAHSEVAHFRKDLGENFKALVLIIFAQYLOQCPEDHVKLVNVEYTEFAKTCVADESAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 144
QY 121 DVNCTAFHNEETFLKKYLYEYIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
DB 145 DVNCTAFHNEETFLKKYLYEYIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 204
QY 181 KLDELDEGKASSAKORLKCASLOKFGERAFAKAWAVARLSORPPKAEFAEVSKLVTDLTK 240
DB 205 KLDELDEGKASSAKORLKCASLOKFGERAFAKAWAVARLSORPPKAEFAEVSKLVTDLTK 264
QY 241 VHTTECHGDLLECCADRADLAKYICENQDSISSKKECEKPLLEKSHCIAEVENDEMPA 300
DB 265 VHTTECHGDLLECCADRADLAKYICENQDSISSKKECEKPLLEKSHCIAEVENDEMPA 324
QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHPDYSVVLRLRAKTYETTTLEKC 360

DB 325 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHPDYSVVLRLRAKTYETTTLEKC 384
QY 361 CAAADPHECYAKVFDEPKPLVEEPQNLIKONCELFQOLGEYKFQNALLYRYTKKVPQVST 420
DB 385 CAAADPHECYAKVFDEPKPLVEEPQNLIKONCELFQOLGEYKFQNALLYRYTKKVPQVST 444
QY 421 PTLVEYSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNOLCVLHEKTPVSDRVTKCCTES 480
DB 445 PTLVEYSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNOLCVLHEKTPVSDRVTKCCTES 504
QY 481 LVNRRPCFSALEVDITYVPKEFNAETTFHADICTLSEKERQIKKQTAIVLVELYKHKPKAT 540
DB 505 LVNRRPCFSALEVDITYVPKEFNAETTFHADICTLSEKERQIKKQTAIVLVELYKHKPKAT 564
QY 541 KEOLKAVMDDDFAAFVEKCKCKADDDKTCFAEEGKKLVAASQAALGL 585
DB 565 KEOLKAVMDDDFAAFVEKCKCKADDDKTCFAEEGKKLVAASQAALGL 609
RESULT 9
US-10-153-064-133
; Sequence 133, Application US/10153064
; Patent No. US20020142814A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 133
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-064-133
Query Match 100.0%; Score 3103; DB 12; Length 651;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAHSEVAHFRKDLGENFKALVLIIFAQYLOQCPEDHVKLVNVEYTEFAKTCVADESAE 60
DB 67 DAHSEVAHFRKDLGENFKALVLIIFAQYLOQCPEDHVKLVNVEYTEFAKTCVADESAE 126
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
DB 127 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 186
QY 121 DVNCTAFHNEETFLKKYLYEYIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
DB 187 DVNCTAFHNEETFLKKYLYEYIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 246
QY 181 KLDELDEGKASSAKORLKCASLOKFGERAFAKAWAVARLSORPPKAEFAEVSKLVTDLTK 240
DB 247 KLDELDEGKASSAKORLKCASLOKFGERAFAKAWAVARLSORPPKAEFAEVSKLVTDLTK 306
QY 241 VHTTECHGDLLECCADRADLAKYICENQDSISSKKECEKPLLEKSHCIAEVENDEMPA 300
DB 307 VHTTECHGDLLECCADRADLAKYICENQDSISSKKECEKPLLEKSHCIAEVENDEMPA 366
QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHPDYSVVLRLRAKTYETTTLEKC 360
DB 367 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHPDYSVVLRLRAKTYETTTLEKC 426
QY 361 CAAADPHECYAKVFDEPKPLVEEPQNLIKONCELFQOLGEYKFQNALLYRYTKKVPQVST 420
DB 427 CAAADPHECYAKVFDEPKPLVEEPQNLIKONCELFQOLGEYKFQNALLYRYTKKVPQVST 486
QY 421 PTLVEYSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNOLCVLHEKTPVSDRVTKCCTES 480

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||||| PTLVEYRNGLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKCCTES 546
Db 487
QY 481 LVNRRPCFSALEVDEYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKPKAT 540
|||||
Db 547 LVNRRPCFSALEVDEYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKPKAT 606
QY 541 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585
|||||
Db 607 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 651

RESULT 10
US-10-153-064-132
; Sequence 132, Application US/10153064
; Patent No. US20020142814A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-064-132

Query Match 100.0%; Score 3103; DB 12; Length 652;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGGENFKALVLI AFAQYLOQCPPEHVKLVNVEYTEFAKTCADESAE 60
|||||
Db 68 DAHKSEVAHRFKDLGGENFKALVLI AFAQYLOQCPPEHVKLVNVEYTEFAKTCADESAE 127
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPNERNECFLOHKDDNPNLRLVRPEV 120
|||||
Db 128 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPNERNECFLOHKDDNPNLRLVRPEV 187
QY 121 DVNCTAFHNEETFLKKLYEIAARRHPYFYAPPELLFAKRYKAAFTCCQAADKAACLLP 180
|||||
Db 188 DVNCTAFHNEETFLKKLYEIAARRHPYFYAPPELLFAKRYKAAFTCCQAADKAACLLP 247
QY 181 KLDELDEGKASSAKQRLKASLOKFGERAFAKAWARLSQRPKAEFAEVSKLVDLTk 240
|||||
Db 248 KLDELDEGKASSAKQRLKASLOKFGERAFAKAWARLSQRPKAEFAEVSKLVDLTk 307
QY 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
|||||
Db 308 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 367
QY 301 DLPSLAADFVESKDVCKNVAEAKDVLGMFLYEYARRHPDYSVVLRLRAKTYETTLK 360
|||||
Db 368 DLPSLAADFVESKDVCKNVAEAKDVLGMFLYEYARRHPDYSVVLRLRAKTYETTLK 427
QY 361 CAAADPHECYAKVDFEFKPLVEEPQNLIKONCELFOLGEYKFNALLVRYTKVPQVST 420
|||||
Db 428 CAAADPHECYAKVDFEFKPLVEEPQNLIKONCELFOLGEYKFNALLVRYTKVPQVST 487
QY 421 PTLVEYSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKCCTES 480
|||||
Db 488 PTLVEYSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKCCTES 547
QY 481 LVNRRPCFSALEVDEYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKPKAT 540
|||||
Db 548 LVNRRPCFSALEVDEYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKPKAT 607
QY 541 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585
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||||| KEQLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 652
Db 608

RESULT 11
US-10-153-064-131
; Sequence 131, Application US/10153064
; Patent No. US20020142814A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-064-131

Query Match 100.0%; Score 3103; DB 12; Length 653;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGGENFKALVLI AFAQYLOQCPPEHVKLVNVEYTEFAKTCADESAE 60
|||||
Db 69 DAHKSEVAHRFKDLGGENFKALVLI AFAQYLOQCPPEHVKLVNVEYTEFAKTCADESAE 128
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPNERNECFLOHKDDNPNLRLVRPEV 120
|||||
Db 129 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPNERNECFLOHKDDNPNLRLVRPEV 188
QY 121 DVNCTAFHNEETFLKKLYEIAARRHPYFYAPPELLFAKRYKAAFTCCQAADKAACLLP 180
|||||
Db 189 DVNCTAFHNEETFLKKLYEIAARRHPYFYAPPELLFAKRYKAAFTCCQAADKAACLLP 248
QY 181 KLDELDEGKASSAKQRLKASLOKFGERAFAKAWARLSQRPKAEFAEVSKLVDLTk 240
|||||
Db 249 KLDELDEGKASSAKQRLKASLOKFGERAFAKAWARLSQRPKAEFAEVSKLVDLTk 308
QY 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
|||||
Db 309 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 368
QY 301 DLPSLAADFVESKDVCKNVAEAKDVLGMFLYEYARRHPDYSVVLRLRAKTYETTLK 360
|||||
Db 369 DLPSLAADFVESKDVCKNVAEAKDVLGMFLYEYARRHPDYSVVLRLRAKTYETTLK 428
QY 361 CAAADPHECYAKVDFEFKPLVEEPQNLIKONCELFOLGEYKFNALLVRYTKVPQVST 420
|||||
Db 429 CAAADPHECYAKVDFEFKPLVEEPQNLIKONCELFOLGEYKFNALLVRYTKVPQVST 488
QY 421 PTLVEYSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKCCTES 480
|||||
Db 489 PTLVEYSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKCCTES 548
QY 481 LVNRRPCFSALEVDEYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKPKAT 540
|||||
Db 549 LVNRRPCFSALEVDEYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKPKAT 608
QY 541 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585
|||||
Db 609 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 653

RESULT 12
US-10-153-064-130
; Sequence 130, Application US/10153064
; Patent No. US20020142814A1
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; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 656
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-064-130

Query Match 100.0%; Score 3103; DB 12; Length 656;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGEENFKALVLIAPFAQYLQOCPPFEDHVKLVNEVTEFAKTCVADESAAE 60
DB 72 DAHKSEVAHRFKDLGEENFKALVLIAPFAQYLQOCPPFEDHVKLVNEVTEFAKTCVADESAAE 131
QY 61 NCKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
DB 132 NCKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 191
QY 121 DVMTAFHDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
DB 192 DVMTAFHDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 251
QY 181 KLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRPKAEFAEVS KLVTDLTK 240
DB 252 KLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRPKAEFAEVS KLVTDLTK 311
QY 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKECCCKPLEKSHCIAEVENDEMPA 300
DB 312 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKECCCKPLEKSHCIAEVENDEMPA 371
QY 301 DLPSLAADFVESKDVCNKYAEAKDVLGMLFYEARRHDPYSVVLLRLAKTYETTTLEKC 360
DB 372 DLPSLAADFVESKDVCNKYAEAKDVLGMLFYEARRHDPYSVVLLRLAKTYETTTLEKC 431
QY 361 CAAADPHECYAKVDFEFPKPLVEEPQNLIKQNCSELFQOLGEYKFQNALLVRYTKKVPQVST 420
DB 432 CAAADPHECYAKVDFEFPKPLVEEPQNLIKQNCSELFQOLGEYKFQNALLVRYTKKVPQVST 491
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 492 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 551
QY 481 LVNRRPCFSALEVDYETVPKFEFNAETFTPHADICTLSEKERQIKKQATLVELVKKHKPKAT 540
DB 552 LVNRRPCFSALEVDYETVPKFEFNAETFTPHADICTLSEKERQIKKQATLVELVKKHKPKAT 611
QY 541 KEQLKAVMDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585
DB 612 KEQLKAVMDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 656

RESULT 13
US-10-153-064-127
; Sequence 127, Application US/10153064
; Patent No. US20020142814A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-064-127

Query Match 100.0%; Score 3103; DB 12; Length 676;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGEENFKALVLIAPFAQYLQOCPPFEDHVKLVNEVTEFAKTCVADESAAE 60
DB 92 DAHKSEVAHRFKDLGEENFKALVLIAPFAQYLQOCPPFEDHVKLVNEVTEFAKTCVADESAAE 151
QY 61 NCKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
DB 152 NCKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 211
QY 121 DVMTAFHDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
DB 212 DVMTAFHDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 271
QY 181 KLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRPKAEFAEVS KLVTDLTK 240
DB 272 KLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRPKAEFAEVS KLVTDLTK 331
QY 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKECCCKPLEKSHCIAEVENDEMPA 300
DB 332 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKECCCKPLEKSHCIAEVENDEMPA 391
QY 301 DLPSLAADFVESKDVCNKYAEAKDVLGMLFYEARRHDPYSVVLLRLAKTYETTTLEKC 360
DB 392 DLPSLAADFVESKDVCNKYAEAKDVLGMLFYEARRHDPYSVVLLRLAKTYETTTLEKC 451
QY 361 CAAADPHECYAKVDFEFPKPLVEEPQNLIKQNCSELFQOLGEYKFQNALLVRYTKKVPQVST 420
DB 452 CAAADPHECYAKVDFEFPKPLVEEPQNLIKQNCSELFQOLGEYKFQNALLVRYTKKVPQVST 511
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 512 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 571
QY 481 LVNRRPCFSALEVDYETVPKFEFNAETFTPHADICTLSEKERQIKKQATLVELVKKHKPKAT 540
DB 572 LVNRRPCFSALEVDYETVPKFEFNAETFTPHADICTLSEKERQIKKQATLVELVKKHKPKAT 631
QY 541 KEQLKAVMDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585
DB 632 KEQLKAVMDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 676

RESULT 14
US-10-153-064-129
; Sequence 129, Application US/10153064
; Patent No. US20020142814A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-064-129

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Query Match      100.0%; Score 3103; DB 12; Length 676;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVHRFKDLGEEFNKALVLIATAFYLOQCFFEDHVKLVNVEVTEFAKTCVADESAAE 60
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DB 92 DAHKSEVHRFKDLGEEFNKALVLIATAFYLOQCFFEDHVKLVNVEVTEFAKTCVADESAAE 151
    |||

QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPMLPRLVRPEV 120
    |||
DB 152 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPMLPRLVRPEV 211
    |||

QY 121 DVMCTAFHDNEETFLKKYLYEIARHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
    |||
DB 212 DVMCTAFHDNEETFLKKYLYEIARHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 271
    |||

QY 181 KLDELDRDGKASSAKQRLKCSLQFGERAFKAWAVARLSORFPKAEVSKLVTDLT 240
    |||
DB 272 KLDELDRDGKASSAKQRLKCSLQFGERAFKAWAVARLSORFPKAEVSKLVTDLT 331
    |||

QY 241 VHTTECHGDLLECADRADLAKYICENODSISKKLKECEKPLLEKSHCIAEVENDEMPA 300
    |||
DB 332 VHTTECHGDLLECADRADLAKYICENODSISKKLKECEKPLLEKSHCIAEVENDEMPA 391
    |||

QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVLLRLAKTYETTLK 360
    |||
DB 392 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVLLRLAKTYETTLK 451
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QY 361 CAADPHCEYAKVDFEPLVEEPONLIKQNCLEFEQLGEYKFNALLVRYTKVPQVST 420
    |||
DB 452 CAADPHCEYAKVDFEPLVEEPONLIKQNCLEFEQLGEYKFNALLVRYTKVPQVST 511
    |||

QY 421 PTLVEVSRNLKGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHBEKTPVSDRVTKCCTES 480
    |||
DB 512 PTLVEVSRNLKGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHBEKTPVSDRVTKCCTES 571
    |||

QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKEROIKKOTALVELVKKHKPKAT 540
    |||
DB 572 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKEROIKKOTALVELVKKHKPKAT 631
    |||

QY 541 KEOLKAVMDDDFAAFVEKCKKADDDKTCFAEBEGKKLVAASQAALGL 585
    |||
DB 632 KEOLKAVMDDDFAAFVEKCKKADDDKTCFAEBEGKKLVAASQAALGL 676
    |||

RESULT 15
US-10-153-064-125
; Sequence 125, Application US/10153064
; Patent No. US20020142814A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 125
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-064-125

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Query Match      100.0%; Score 3103; DB 12; Length 677;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVHRFKDLGEEFNKALVLIATAFYLOQCFFEDHVKLVNVEVTEFAKTCVADESAAE 60
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DB 93 DAHKSEVHRFKDLGEEFNKALVLIATAFYLOQCFFEDHVKLVNVEVTEFAKTCVADESAAE 152
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QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPMLPRLVRPEV 120
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QY 121 DVMCTAFHDNEETFLKKYLYEIARHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
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DB 213 DVMCTAFHDNEETFLKKYLYEIARHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 272
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QY 181 KLDELDRDGKASSAKQRLKCSLQFGERAFKAWAVARLSORFPKAEVSKLVTDLT 240
    |||
DB 273 KLDELDRDGKASSAKQRLKCSLQFGERAFKAWAVARLSORFPKAEVSKLVTDLT 332
    |||

QY 241 VHTTECHGDLLECADRADLAKYICENODSISKKLKECEKPLLEKSHCIAEVENDEMPA 300
    |||
DB 333 VHTTECHGDLLECADRADLAKYICENODSISKKLKECEKPLLEKSHCIAEVENDEMPA 392
    |||

QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVLLRLAKTYETTLK 360
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DB 393 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVLLRLAKTYETTLK 452
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QY 361 CAADPHCEYAKVDFEPLVEEPONLIKQNCLEFEQLGEYKFNALLVRYTKVPQVST 420
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DB 453 CAADPHCEYAKVDFEPLVEEPONLIKQNCLEFEQLGEYKFNALLVRYTKVPQVST 512
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QY 421 PTLVEVSRNLKGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHBEKTPVSDRVTKCCTES 480
    |||
DB 513 PTLVEVSRNLKGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHBEKTPVSDRVTKCCTES 572
    |||

QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKEROIKKOTALVELVKKHKPKAT 540
    |||
DB 573 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKEROIKKOTALVELVKKHKPKAT 632
    |||

QY 541 KEOLKAVMDDDFAAFVEKCKKADDDKTCFAEBEGKKLVAASQAALGL 585
    |||
DB 633 KEOLKAVMDDDFAAFVEKCKKADDDKTCFAEBEGKKLVAASQAALGL 677
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Search completed: April 24, 2003, 07:41:08
Job time : 267 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 24, 2003, 07:22:18 ; Search time 21 Seconds
(without alignments)
2678.030 Million cell updates/sec

Title: US-09-833-111-18

Perfect score: 3103

Sequence: 1 DAHSEVAHREFKDLGEENFK.....TCFAEGKKLVAASQAALGL 585

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3103	100.0	609	1 ABHUS	serum albumin prec
2	2942	94.8	609	2 A47391	serum albumin prec
3	2620	84.4	608	2 S57632	serum albumin prec
4	2475.5	79.8	607	1 ABHOS	serum albumin prec
5	2446.5	78.8	607	1 ABHOS	serum albumin prec
6	2432.5	78.4	607	1 ABHOS	serum albumin prec
7	2426	78.2	608	1 ABHOS	serum albumin prec
8	2411.5	77.7	605	1 ABPGS	serum albumin prec
9	2387	76.9	609	2 JC5838	albumin - Mongolia
10	1861	60.0	453	2 A05139	serum albumin - mo
11	1557.5	50.2	615	1 ABCHS	serum albumin prec
12	1253.5	40.4	609	2 JC4258	alpha-fetoprotein
13	1249.5	40.3	609	1 FPHU	alpha-fetoprotein
14	1242.5	40.0	609	1 FPGO	alpha-fetoprotein
15	1205	38.8	607	1 ABLX72	74K albumin prec
16	1181.5	38.1	265	2 I46986	albumin - dog (fra
17	1175.5	37.9	608	1 ABLX68	68K serum albumin
18	1084	34.9	605	1 FPM5	alpha-fetoprotein
19	1067	34.4	611	1 FPHU	alpha-fetoprotein
20	1055	34.0	599	1 A54906	afamin precursor -
21	928.5	29.9	614	2 S59517	serum albumin prec
22	928	29.9	608	2 A53195	afamin precursor -
23	747.5	24.1	608	1 ABONS1	serum albumin 1 pr
24	742.5	23.9	608	1 ABONS2	serum albumin 2 pr
25	699	22.5	382	2 A37253	serum albumin - bu
26	440.5	14.2	1423	1 S27941	serum albumin - se
27	386	12.4	474	1 VYHUI	vitamin D-binding
28	385	12.4	476	1 VVRTD	vitamin D-binding
29	372	12.0	472	1 A35327	vitamin D-binding

ALIGNMENTS

RESULT 1

ABHUS

serum albumin precursor [validated] - human

N:Alternate names: preproalbumin

N:Contains: kinetensin

C:Species: Homo sapiens (man)

C:Date: 29-Jul-1981 #sequence_revision 31-Jan-1997 #text_change 17-Mar-2000

C:Accession: A93743; A93936; I39427; I59286; I59313; G01747; S55314; A91420; S06422;

R:Lawn, R.M.; Adelman, J.; Bock, S.C.; Franke, A.E.; Houlck, C.M.; Najarian, R.C.; See

Nucleic Acids Res. 9, 6103-6114, 1981

A:Title: The sequence of human serum albumin cDNA and its expression in Escherichia c

A:Reference number: A93743; MUID:82081882; PMID:6171778

A:Accession: A93743

A:Molecule type: mRNA

A:Residues: 1-419, 'K', 421-609 <LAW>

A:Cross-references: EMBL:V00495; GB:J00078; GB:L00132; GB:L00133; NID:g28591; PIDN:CA

R:Dugaiczyk, A.; Law, S.W.; Dennison, O.E.

Proc. Natl. Acad. Sci. U.S.A. 79, 71-75, 1982

A:Title: Nucleotide sequence and the encoded amino acids of human serum albumin mRNA.

A:Reference number: A93936; MUID:82105994; PMID:6275391

A:Accession: A93936

A:Molecule type: mRNA

A:Residues: 1-120, 'G', 122-609 <DUG>

A:Cross-references: EMBL:V00494; NID:g28589; PIDN:CAA23753.1; PID:g28590

R:Urano, Y.; Watanabe, K.; Sakai, M.; Tamaoki, T.

J. Biol. Chem. 261, 3244-3251, 1986

A:Title: The human albumin gene. Characterization of the 5' and 3' flanking regions a

A:Reference number: I39427; MUID:86140099; PMID:2419329

A:Accession: I39427

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-26 <URA>

A:Cross-references: GB:M13075; NID:g178330; PIDN:AAA51688.1; PID:g553173

R:Watkins, S.; Madison, J.; Galliano, M.; Minchiotti, L.; Putnam, F.W.

Proc. Natl. Acad. Sci. U.S.A. 91, 2275-2279, 1994

A:Title: A nucleotide insertion and frameshift cause analbuminemia in an Italian fami

A:Reference number: I59286; MUID:94181575; PMID:8134387

A:Accession: I59286

A>Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 282-290, 'KSRFDLO', <WAT>

A:Cross-references: GB:S69192; NID:g546032; PIDN:AAB30282.1; PID:g546033

A>Note: This frame-shift variant, designated albumin Roma, leads to analbuminemia

R:Madison, J.; Galliano, M.; Watkins, S.; Minchiotti, L.; Porta, F.; Rossi, A.; Putna

Proc. Natl. Acad. Sci. U.S.A. 91, 6476-6480, 1994

A:Title: Genetic variants of human serum albumin in Italy: point mutants and a carbox

A:Reference number: I59313; MUID:94294404; PMID:8022807

A:Accession: I59313

A>Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 589-590, 'ALPRRVKMLLLQVKLP', <MAD>

A:Cross-references: GB:S70799; NID:g547231; PIDN:AAB31177.1; PID:g547232

cag island protein
cag pathogenicity
calcium-binding pr
hypothetical prote
major surface glyco
cell surface glyco
hypothetical prote
hypothetical prote
sperm tail-specifi
kinesin homolog P2
major surface glyco
myosin heavy chain
cell-cycle-depende
glycoprotein A - P
hypothetical prote
giantin - human
embryonic muscle m

A>Note: this frame-shift variant is designated albumin Bazzano; four additional variants
R:Menaya, J.; Parrilla, R.; Ayuso, M.S.
submitted to the EMBL Data Library, March 1995
A:Reference number: G08292
A:Accession: G01747
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-120, 'G', 122-455 <MEN>
A:Cross-references: EMBL:U22961; NID:G763428; PIDN:AAA64922.1; PID:G763431
R:Ledgerwood, E.C.; George, P.M.; Peach, R.J.; Brennan, S.O.
Biochem. J. 308, 321-325, 1995
A>Title: Endoproteolytic processing of recombinant proalbumin variants by the yeast *Kex2*
A:Reference number: S55314; MUID:95275251; PMID:7755581
A:Accession: S55314
A:Molecule type: protein
A:Residues: 19-27 <LED>
R:Meloun, B.; Moravsek, L.; Kostka, V.
FEBS Lett. 58, 134-137, 1975
A>Title: Complete amino acid sequence of human serum albumin.
A:Reference number: A91420; MUID:76187907; PMID:1225573
A:Accession: A91420
A:Molecule type: protein
A:Residues: 25-117, 'EQ', 120-154, 'Q', 156-193, 'E', 195-387, 'H', 389-390, 'Y', 392-393, 'A', 395-
R:Roehr, U.; Spitteller, G.; Tripter, D.
Justus Liebig's Ann. Chem. 9, 881-884, 1988
A>Title: Isolation and structure elucidation of middle-molecular weight peptides from ur
A:Reference number: S06422
A>Note: this paper is in German, with an English abstract
A:Accession: S06422
A:Molecule type: protein
A:Residues: 25-48 <ROE>
R:Finch, J.W.; Crouch, R.K.; Knapp, D.R.; Schey, K.L.
Arch. Biochem. Biophys. 305, 595-599, 1993
A>Title: Mass spectrometric identification of modifications to human serum albumin treat
A:Reference number: S36882; MUID:93384321; PMID:8373198
A:Accession: S36882
A:Molecule type: protein
A:Residues: 45-67, 141-160, 311-337, 469-490, 570-581 <FIN>
R:Kausler, E.; Spitteller, G.
Biol. Chem. Hoppe-Seyler 372, 849-855, 1991
A>Title: Bruchstuecke aus Albumin und beta(2)-Mikroglobulin - Bestandteile der Mittelmol
A:Reference number: S17599; MUID:92126241; PMID:1772598
A:Accession: S17599
A:Molecule type: protein
A:Residues: 25-54, 354-357, 431-447 <KAU>
A>Note: 49-Leu was also found
R:Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A>Title: Structures of histamine-releasing peptides formed by the action of acid proteas
A:Reference number: A45800; MUID:89341406; PMID:2474609
A:Accession: A45800
A:Molecule type: protein
A:Residues: 166-173 <CAR>
R:Mogard, M.H.; Kobayashi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; Wa
Biochem. Biophys. Res. Commun. 136, 983-988, 1986
A>Title: The amino acid sequence of kinetensin, a novel peptide isolated from pepsin-tre
A:Reference number: A03239; MUID:86242180; PMID:3087352
A:Accession: A03239
A:Molecule type: protein
A:Residues: 166-173, 'L' <MOG>
R:Galliano, M.; Minchiotti, L.; Porta, F.; Rossi, A.; Ferri, G.; Madison, J.; Watkins, S
Proc. Natl. Acad. Sci. U.S.A. 87, 8721-8725, 1990
A>Title: Mutations in genetic variants of human serum albumin found in Italy.
A:Reference number: A38255; MUID:91062352; PMID:2247440
A:Accession: C38255
A:Molecule type: protein
A:Residues: 76-111 <GAL>
A:Accession: B38255
A:Molecule type: protein
A:Residues: 82-105, 'K', 107-110 <GAL2>
A>Note: this variant is designated albumin Vibo Valentia
A:Accession: A38255
A:Molecule type: protein

A:Residues: 76-83, 'K', 85-106 <GAL3>
A>Note: this variant is designated albumin Torino
R:Minchiotti, L.; Galliano, M.; Zapponi, M.C.; Tenni, R.
Eur. J. Biochem. 214, 437-444, 1993
A>Title: The structural characterization and bilirubin-binding properties of albumin
A:Reference number: S33298; MUID:93292504; PMID:8513793
A:Accession: S33298
A:Molecule type: protein
A:Residues: 255-263, 'E', 265-281 <MIN1>
A>Note: this variant is designated albumin Herborn
R:Minchiotti, L.; Galliano, M.; Stoppini, M.; Ferri, G.; Crespeau, H.; Rochu, D.; Por
Biochim. Biophys. Acta 1119, 232-238, 1992
A>Title: Two albumins with identical electrophoretic mobility are produced by dif
A:Reference number: S21078; MUID:92190239; PMID:1347703
A:Accession: S21078
A:Molecule type: protein
A:Residues: 354-356, 'K', 358-378 <MIN2>
A>Note: this variant is designated albumin Sondrio; another variant Paris-2 is report
R:He, X.M.; Carter, D.C.
Nature 358, 209-215, 1992
A>Title: Atomic structure and chemistry of human serum albumin.
A:Reference number: A46756; MUID:92334427; PMID:1630489
A:Contents: annotation; X-ray crystallography, 2.8 angstroms
R:Brown, J.R.; Shockley, P.; Behrens, P.Q.
In The Chemistry and Physiology of the Human Plasma Proteins, Bing, D.H., ed., pp. 23-
A:Reference number: A9442
A:Contents: annotation; three-dimensional structure and disulfide bonds
R:Saber, M.A.; Stockbauer, P.; Moravsek, L.; Meloun, B.
Collect. Czech. Chem. Commun. 42, 564-579, 1977
A>Title: Disulfide bonds in human serum albumin.
A:Reference number: A90930
A:Contents: annotation; disulfide bonds
R:Jacobsen, C.
Biochem. J. 171, 453-459, 1978
A>Title: Lysine residue 240 of human serum albumin is involved in high-affinity bindi
A:Reference number: A90299; MUID:78186630; PMID:656055
A:Contents: annotation; bilirubin-binding site
R:Petters, T.; Reed, R.G.
In Albumin: Structure, Biosynthesis, Function, Peters, J., and Sjöholm, I., eds., 11-
A>Title: Serum albumin: conformation and active sites.
A:Reference number: A94408
A:Contents: annotation; binding sites
R:Harper, M.E.; Dugaiczky, A.
Am. J. Hum. Genet. 35, 565-572, 1983
A>Title: Linkage of the evolutionarily-related serum albumin and alpha-fetoprotein ge
A:Reference number: A90028; MUID:83279982; PMID:6192711
A:Contents: annotation; gene position
R:Walker, J.E.
FEBS Lett. 66, 173-175, 1976
A>Title: Lysine residue 199 of human serum albumin is modified by acetylsalicylic ac
A:Reference number: A46755; MUID:76257808; PMID:955075
A:Contents: annotation
A>Note: the nonenzymatic transfer of an acetyl group from aspirin (acetylsalicylic a
R:Bohney, J.P.; Fonda, M.L.; Feldhoff, R.C.
FEBS Lett. 298, 266-268, 1992
A>Title: Identification of Lys(190) as the primary binding site for pyridoxal 5'-phos
A:Reference number: A56294; MUID:92183881; PMID:1544460
A:Contents: annotation
A>Note: the nonenzymatic binding of pyridoxal phosphate to lysine-214 is described; 1
atase activity
C:Comment: Serum albumin, a predominant protein in the plasma of adults, is synthesiz
lirubin, protoporphyrin, long-chain fatty acids, prostaglandins, steroid hormones (we
C:Comment: A large number of variants of human serum albumin have been described.
C:Genetics:
A:Gene: GDB:ALB
A:Cross-references: GDB:118990; OMIM:103600
A:Map position: 4q11-4q13
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; duplication; metal binding; phosphoprotein; plasma; pyr
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-24/Domain: propeptide #status experimental <PRO>
F:25-609/Product: serum albumin #status experimental <MPT>
F:29-202/Domain: serum albumin repeat homology <SAL>

F:166-174/Product: kinetensin #status experimental <KIP>
 F:221-394/Domain: serum albumin repeat homology <SA2>
 F:413-592/Domain: serum albumin repeat homology <SA2>
 F:27/Binding site: copper (His) #status predicted
 F:77-86,99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-385,384-393,4
 F:214/Binding site: pyridoxal phosphate (lys) (covalent) #status experimental

Query Match 100.0%; Score 3103; DB 1; Length 609;
 Best Local Similarity 100.0%; Pred. No. 7.4e-198;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRKDLGEENFKALVLIATAFYQYLOQCFFEDHVKLVNVEVTEFAKTCVADESAB 60
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 Qy 61 NCDKSLHLTFLGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRVPEV 120
 Db 85 NCDKSLHLTFLGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRVPEV 144
 Qy 121 DVMTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
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 Qy 241 VHTECHGDLLECADRADLAKYICENQDSISSKLKCECEKPLLEKSHCIAEVENDEMPA 300
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 Db 325 DLPSLAADFEVSKDCKNYAEAKDVLGMFLYFYARRHPDYSVLLLRLLAKTYETTLK 384
 Qy 361 CAADPHCYAKVDFEPLVEEPQNLKQNCLEFEQGEYKFNALLVRYTKKVPQVST 420
 Db 385 CAADPHCYAKVDFEPLVEEPQNLKQNCLEFEQGEYKFNALLVRYTKKVPQVST 444
 Qy 421 PTLVSVNLGKVGSKCKHPEAKRMPCAEDYLSVVLNOLCVLHKTVPDSRVTKCCTES 480
 Db 445 PTLVSVNLGKVGSKCKHPEAKRMPCAEDYLSVVLNOLCVLHKTVPDSRVTKCCTES 504
 Qy 481 LVNRRPCFSALVEVDYTPKFEKNAETFTFHADICTLSEKEROIKKQKOTALVELVKKHPRAT 540
 Db 505 LVNRRPCFSALVEVDYTPKFEKNAETFTFHADICTLSEKEROIKKQKOTALVELVKKHPRAT 564
 Qy 541 KEQLKAVMDDFAAFEVKCKKADDKETCTFAEKGKLVVAASQAALGL 585
 Db 565 KEQLKAVMDDFAAFEVKCKKADDKETCTFAEKGKLVVAASQAALGL 609

RESULT 2
 A:7391
 serum albumin precursor - rhesus macaque
 C:Species: Macaca mulatta (rhesus macaque)
 C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
 C:Accession: A47391
 R:Watkins, S.; Sakamoto, Y.; Madison, J.; Davis, E.; Smith, D.G.; Dwulet, J.; Putnam, F.
 Proc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993
 A:Title: cDNA and protein sequence of polymorphic macaque albumins that differ in bilirubin binding site
 A:Reference number: A47391; MUID:93211971; PMID:8460152
 A:Contents: B/B homozygote
 A:Accession: A47391
 A:Status: preliminary
 A:Molecule type: mRNA; protein
 A:Residues: 1-600 <WAT>
 A:Cross-references: GB:M90463; NID:g342294; PIDN:AAA36906.1; PID:g342295
 A:Experimental source: liver
 A:Note: sequence extracted from NCBI backbone (NCBIN:128280, NCBIP:128281)
 C:Superfamily: serum albumin; serum albumin repeat homology
 F:21-194/Domain: serum albumin repeat homology <SA1>
 F:213-386/Domain: serum albumin repeat homology <SA2>

F:405-584/Domain: serum albumin repeat homology <SA3>
 Query Match 94.8%; Score 2942; DB 2; Length 600;
 Best Local Similarity 93.5%; Pred. No. 3.3e-187;
 Matches 545; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRKDLGEENFKALVLIATAFYQYLOQCFFEDHVKLVNVEVTEFAKTCVADESAB 60
 Db 17 DTHKSEVAHRKDLGEENFKGLVLFVAFSOLQOCFFEEHVKLVNVEVTEFAKTCVADESAB 76
 Qy 61 NCDKSLHLTFLGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRVPEV 120
 Db 77 NCDKSLHLTFLGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRVPEV 136
 Qy 121 DVMTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
 Db 137 DVMTAFHDNEATFLKKYLYEVARRRHPYFYAPPELLFFAARYKAAFAECCQAAADKAACLLP 196
 Qy 181 KLDELDRGKASSAKQRLKASLQKFGFRKAWAVARLSQRPKAEFAEVSCLVTDLT 240
 Db 197 KLDELDRGKASSAKQRLKASLQKFGFRKAWAVARLSQRPKAEFAEVSCLVTDLT 256
 Qy 241 VHTECHGDLLECADRADLAKYICENQDSISSKLKCECEKPLLEKSHCIAEVENDEMPA 300
 Db 257 VHTECHGDLLECADRADLAKYICENQDSISSKLKCECEKPLLEKSHCIAEVENDEMPA 316
 Qy 301 DLPSLAADFEVSKDCKNYAEAKDVLGMFLYFYARRHPDYSVLLLRLLAKTYETTLK 360
 Db 317 DLPSLAADFEVSKDCKNYAEAKDVLGMFLYFYARRHPDYSVLLLRLLAKTYETTLK 376
 Qy 361 CAADPHCYAKVDFEPLVEEPQNLKQNCLEFEQGEYKFNALLVRYTKKVPQVST 420
 Db 377 CAADPHCYAKVDFEPLVEEPQNLKQNCLEFEQGEYKFNALLVRYTKKVPQVST 436
 Qy 421 PTLVSVNLGKVGSKCKHPEAKRMPCAEDYLSVVLNOLCVLHKTVPDSRVTKCCTES 480
 Db 437 PTLVSVNLGKVGSKCKHPEAKRMPCAEDYLSVVLNOLCVLHKTVPSEKVTCCCTES 496
 Qy 481 LVNRRPCFSALVEVDYTPKFEKNAETFTFHADICTLSEKEROIKKQKOTALVELVKKHPRAT 540
 Db 497 LVNRRPCFSALVEDEAYVPRAFNAETFTFHADMCTLSEKROKQKOTALVELVKKHPRAT 556
 Qy 541 KEQLKAVMDDFAAFEVKCKKADDKETCTFAEKGKLVVAASQAAL 583
 Db 557 KEQLKAVMDNFPAFEVKCKKADDKETCTFAEKGKLVVAASQAAL 599

RESULT 3
 S57632
 serum albumin precursor - cat
 C:Species: Felis silvestris catus (domestic cat)
 C:Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Aug-1999
 C:Accession: J04660; S57632
 R:Hilger, C.; Grigioni, F.; Hentges, F.
 Gene 169, 295-296, 1996
 A:Title: Sequence of the gene encoding cat (Felis domesticus) serum albumin.
 A:Reference number: J04660; MUID:96194824; PMID:8647469
 A:Accession: J04660
 A:Molecule type: mRNA
 A:Residues: 1-608 <HI2>
 A:Cross-references: EMBL:X84842; NID:g886484; PIDN:CAA59279.1; PID:g886485
 A:Experimental source: liver
 C:Comment: This protein is the major protein component in plasma. It functions as a
 ein has 35 conserved cysteine residues.
 C:Superfamily: serum albumin; serum albumin repeat homology
 C:Keywords: liver; plasma
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PRP>
 F:25-608/Product: serum albumin #status predicted <WAT>
 F:221-394/Domain: serum albumin repeat homology <SA1>
 F:221-394/Domain: serum albumin repeat homology <SA2>
 F:413-592/Domain: serum albumin repeat homology <SA3>

A;Residues: 1-32 <MAG>
R;Hsieh, J.C.; Lin, F.P.; Tam, M.F.
Anal. Biochem. 170, 1-8, 1988
A;Title: Electrophoretic transfer filter from an analytical isoelectrofocusing gel
A;Reference number: A60808; MUID:88267456; PMID:3389500
A;Accession: B60808
A;Molecule type: protein
A;Residues: 25-41 <HSI>
R;Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albumin
A;Reference number: S10780; MUID:90336641; PMID:2379503
A;Accession: S10780
A;Molecule type: protein
A;Residues: 25-41, 'H', '43-57, 59-64 <STR>
R;Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A;Title: Structures of histamine-releasing peptides formed by the action of acid proteases
A;Reference number: A45800; MUID:89341406; PMID:2474609
A;Accession: A45800
A;Molecule type: protein
A;Residues: 163-172 <CAR>
R;Carraway, R.E.; Mitra, S.P.; Cochrane, D.E.
J. Biol. Chem. 262, 5968-5973, 1987
A;Title: Structure of a biologically active neurotensin-related peptide obtained from pe
A;Reference number: A26693; MUID:87194805; PMID:2437111
A;Accession: A26693
A;Molecule type: protein
A;Residues: 165-172, 'L', 'CA2>
R;Reed, R.G.; Putnam, F.W.; Peters Jr., T.
Biochem. J. 191, 867-868, 1980
A;Title: Sequence of residues 400-403 of bovine serum albumin.
A;Reference number: A90309; MUID:82023364; PMID:7283978
A;Accession: A90309
A;Molecule type: protein
A;Residues: 402-433 <REE>
R;Brown, J.R.
Fed. Proc. 34, 591, 1975
A;Title: Structure of bovine serum albumin.
A;Reference number: A91458
A;Accession: A91458
A;Molecule type: protein
A;Residues: 25-41, 'H', '43-117, 'EQ', '120-179, 181-189, 'E', '191-194, 'A', '196-213, 'T', '215-288, 'H'
R;Brown, J.R.
submitted to the Atlas, April 1975
A;Reference number: A94551
A;Accession: A94551
A;Molecule type: protein
A;Residues: 190-195 <BR2>
R;Brown, J.R.
Fed. Proc. 33, 1389, 1974
A;Reference number: A91457
A;Contents: annotation; disulfide bonds
R;Werlen, R.C.; Offord, R.E.; Rose, K.
Biochem. J. 302, 907-911, 1994
A;Title: Preparation and characterization of novel substrates of insulin proteinase (EC
A;Reference number: S55232; MUID:95031935; PMID:7945219
A;Accession: S55232
A;Status: preliminary
A;Molecule type: protein
A;Residues: 529-536;569-572 <WER>
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; copper binding; duplication; plasma
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-607/Product: serum albumin #status experimental <MPT>
F;29-201/Domain: serum albumin repeat homology <SAL>
F;220-393/Domain: serum albumin repeat homology <SA2>
F;412-591/Domain: serum albumin repeat homology <SA3>
F;27/Binding site: copper (His) #status predicted
F;77-86, 99-115, 114-125, 147-192, 191-200, 223-269, 268-276, 288-302, 301-312, 339-384, 383-392, 4

Query Match

78.8%; Score 2446.5; DB 1; Length 607;

Best Local Similarity 75.6%; Pred. No. 2.1e-154;
Matches 441; Conservative 71; Mismatches 70; Indels 1; Gaps 1;
QY 1 DAHKSEVAHFRKDLGEENFKALVIAFAQYLOQCFFDHVKLVNEVTEFAKTCVADSEAE 60
DB 25 DTHKSEIAHFRKDLGEQFKGLVIAFSQYLOQCFFDHVKLVNELTEFAKTCVADSEHA 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLPLRVPEV 120
DB 85 GCEKSLHTLFGDELCKVASLRETYGDMADCCKEQEPERNECFLSHKDDSPDLPLK-KPDP 143
QY 121 DVMCTAPHDNEETFLKYLIEIARRHPYFYAPELLFFAKRYKAAFTCCQAADRAACLLP 180
DB 144 NTLCDPEKADKKFKWGLYIEIARRHPYFYAPELLFYANKYNGVFOCCQAEKDGACLLP 203
QY 181 KLDELDEGRKASSAKQRLKCAQKFCGERAFKAWARLQRRFPKAEFAEYSLKLVDTLTK 240
DB 204 KIETMRKVLASSARQRLKCAQKFCGERALKAWARLQRRFPKAEFEVETKLVDTLTK 263
QY 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLEKCEKPLLEKSHCSHAENVDEMPA 300
DB 264 VHKCCCHGDLLECADRADLAKYICDNQDTISSKLEKCEKPLLEKSHCSHAENVKDAIPE 323
QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYIEYARRHPDYSSVLLRLAKYETTTLEKC 360
DB 324 NLPLPLTADFAEDKDYCKNYQEAQDAFLGSLYIEYSRHPYAVSVLLRLAKYETATLEEC 383
QY 361 CAADPHCEYAKVDFEPKPLVEEPQNLKONCELFEOGLGEYKFNALLVRYTKKVPQVST 420
DB 384 CAKDDPHACYSTVPDFKLUHLVDEPNLKNQDQFEKLGEGYFNALLVRYTKKVPQVST 443
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEYDLSVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 444 PTLVEVSRNLGKVGTRCCTKPESEMPCTEDYLSILNRLCVLHEKTPVSEKVKCCTES 503
QY 481 LVNRRPCFSALEVDVTPKFEFNAETFTFHADICTLSEKERQIKKQALVLEKHKPKAT 540
DB 504 LVNRRPCFSALTDPETVVPKAFDEKFTFHADICTLSEKERQIKKQALVLEKHKPKAT 563
QY 541 KEQLKAVMDDFAFVEKCCADDDKCTCFAGEGKLVAAASQAL 583
DB 564 EEQLKTVMENFVAFVDKCCADDDKCTCFAGEGKLVVSTQAL 606

RESULT 6

ABSHS

serum albumin precursor - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999

C;Accession: S06936

R;Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.

Nucleic Acids Res. 17, 10495, 1989

A;Title: Nucleotide and deduced amino acid sequence of sheep serum albumin.

A;Reference number: S06936; MUID:90098888; PMID:2602160

A;Accession: S06936

A;Molecule type: mRNA

A;Residues: 1-607 <BRO>

A;Cross-references: EMBL:X17055; NID:q1386; PIDN:CAA34903.1; PID:q1387

C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper teroid hormones (weak bonds with these hormones promote their transfer across the membrane). Superfamily: serum albumin; serum albumin repeat homology

C;Keywords: carrier protein; duplication; metal binding; plasma

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-24/Domain: propeptide #status predicted <PRO>

F;25-607/Product: serum albumin #status predicted <MAT>

F;29-201/Domain: serum albumin repeat homology <SAL>

F;220-393/Domain: serum albumin repeat homology <SA2>

F;412-591/Domain: serum albumin repeat homology <SA3>

F;27/Binding site: copper (His) #status predicted

F;77-86, 99-115, 114-125, 147-192, 191-200, 223-269, 268-276, 288-302, 301-312, 339-384, 383-392, 4

Query Match

78.4%; Score 2432.5; DB 1; Length 607;

Best Local Similarity 75.0%; Pred. No. 1.8e-153;
Matches 437; Conservative 73; Mismatches 72; Indels 1; Gaps 1;

QY 1 DAHKEVAHFRKDLGEENFKALVLIATAFYLOQCPEFHVHKLNVETFAKTCVADESA 60
Db 25 DTHKEIAHFRKDLGEENFKALVLIATAFYLOQCPEFHVHKLNVETFAKTCVADESA 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPEKNECFLOHKKDNPRLVPRPEV 120
Db 85 GCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPEKNECFLOHKKDNPRLVPRPEV 143
QY 121 DVNCTAFHNEETFLKKYLYEIAARRHPYFAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
Db 144 DTLCAEFKADKFKWGLYEVARRHPYFAPPELLYANKYNGVFQECQAEDKAGACLLP 203
QY 181 KLDELDECKKASSAKORLKASQKGERAFKAWARLVSORFPKAEFAEVSCLVTLDTLK 240
Db 204 KIDAMREKVLASSARQLRCASQKGERALKAWARLVSQKPKADFTDVTXIVTDLTK 263
QY 241 VHTCECHGDLLECCADRADLAKYICENQDSISSKLEKCECKPLEKSHCHIAEYVNDMPA 300
Db 264 VHKCECHGDLLECCADRADLAKYICDHQDALSLSKLEKCECKPVLKSHCHIAEYVNDMPA 323
QY 301 DLPSLAADFVESKDVCKNAEAKDVLGMLFYEYARRHPDYSVLLRLAKTYETTLK 360
Db 324 NLPLTADEADKVEKCNKYEAKDVLGMLFYEYARRHPDYSVLLRLAKTYETTLK 383
QY 361 CAADPHCYAKVDFEKLVEPQNLKONCELFQOLGEYKFNALLVRYTKVQVST 420
Db 384 CAEDPHCYAKVDFEKLVEPQNLKONCELFQOLGEYKFNALLVRYTKVQVST 443
QY 421 PTLVEYSRLNGLKVGSKCKHPEAKRMPCAEDYLSVNLCLVLEHTPTVSDRYTKCTES 480
Db 444 PTLVEYSRLNGLKVGSKCKHPEAKRMPCAEDYLSVNLCLVLEHTPTVSDRYTKCTES 503
QY 481 LVNRFCFSALEVDETVYVPKFEAETFTTHADICTLSEKRIKKTALVELVKKHKKPAT 540
Db 504 LVNRFCFSALEVDETVYVPKFEAETFTTHADICTLSEKRIKKTALVELVKKHKKPAT 563
QY 541 KEOLKAVMDDFAEVKECKCKADKKECFKAEKGLKVAASQAAL 583
Db 564 DEQLKTMENFVAVDKCAADKKEGCFVLEGPKLVAASQAAL 606

RESULT 7
ABRTS
serum albumin precursor - rat
N:Alternate names: preproalbumin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-May-1979 #sequence revision 31-May-1979 #text change 22-Jun-1999
C:Accession: A93872; A92211; A91946; A91940; C45800; I57621; A03233
R:Sargent, T.D.; Yang, M.; Bonner, J.
Proc. Natl. Acad. Sci. U.S.A. 78, 243-246, 1981
A:Title: Nucleotide sequence of cloned rat serum albumin messenger RNA.
A:Reference number: A93872; MUID:81223722; PMID:7017712
A:Accession: A93872
A:Molecule type: mRNA
A:Residues: 1-608 <SAR>
A:Cross-references: GB:J00698; NID:g55627; PIDN:CAA24532.1; PID:g55628
R:Strauss, A.W.; Bennett, C.D.; Donohue, A.M.; Rodkey, J.A.; Alberts, A.W.
J. Biol. Chem. 252, 6846-6855, 1977
A:Title: Rat liver pre-proalbumin: complete amino acid sequence of the pre-piece. Analysis
A:Reference number: A92211; MUID:77249657; PMID:893447
A:Note: cleavages during protein maturation
A:Accession: A92211
A:Molecule type: protein
A:Residues: 1-38 <STR>
R:Isemura, S.; Ikenaka, T.
J. Biochem. 83, 35-48, 1978
A:Title: Amino acid sequences of fragments I and II obtained by cyanogen bromide cleavage
A:Reference number: A91946; MUID:78109429; PMID:564345
A:Accession: A91946
A:Molecule type: protein

A:Residues: 25-222 <ISL>
R:Isemura, S.; Ikenaka, T.
J. Biochem. 79, 1183-1196, 1976
A:Title: Fragmentation of rat serum albumin by cyanogen bromide cleavage and the amino
A:Reference number: A91940; MUID:76260153; PMID:956149
A:Accession: A91940
A:Molecule type: protein
A:Residues: 223-288; 572-608 <IS2>
A:Note: 262-Leu was also found
R:Aoyagi, Y.; Ikenaka, T.; Ichida, F.
Cancer Res. 38, 3483-3486, 1978
A:Title: Copper(II)-binding ability of human alpha-fetoprotein.
A:Reference number: A90758; MUID:79001617; PMID:80265
A:Contents: annotation; copper binding
R:Carraway, R.E.; Cochran, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A:Title: Structures of histamine-releasing peptides formed by the action of acid-proteolysis
A:Reference number: A45800; MUID:89341406; PMID:2474609
A:Accession: C45800
A:Status: preliminary
A:Molecule type: protein
A:Residues: 166-173 <CAR>
R:Heard, J.
Mol. Cell. Biol. 7, 2425-2434, 1987
A:Title: Determinants of rat albumin promoter tissue specificity analyzed by an improved
A:Reference number: I57621; MUID:87286876; PMID:3475566
A:Accession: I57621
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M16825; NID:g202828; PIDN:AAA40712.1; PID:g554412
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; duplication; metal binding; plasma
F:19-24/Domain: signal sequence #status experimental <SIG>
F:25-608/Product: serum albumin #status experimental <PRO>
F:221-394/Domain: serum albumin repeat homology <SA1>
F:413-592/Domain: serum albumin repeat homology <SA2>
F:27/Binding site: copper (His) #status experimental
F:77-86,99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-385,384-393

Query Match 78.2%; Score 2426; DB 1; Length 608;
Best Local Similarity 73.4%; Pred. No. 4.7e-153;
Matches 428; Conservative 82; Mismatches 73; Indels 0; Gaps 0;

QY 1 DAHKEVAHFRKDLGEENFKALVLIATAFYLOQCPEFHVHKLNVETFAKTCVADESA 60
Db 25 EAHKEIAHFRKDLGEENFKALVLIATAFYLOQCPEFHVHKLNVETFAKTCVADENA 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPEKNECFLOHKKDNPRLVPRPEV 120
Db 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPEKNECFLOHKKDNPRLVPRPEV 144
QY 121 DVNCTAFHNEETFLKKYLYEIAARRHPYFAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
Db 145 EAMCTSFQENPTSFGLHYLHEVARRHPYFAPPELLYAEKYNEVLTQCCTESDKAACLTP 204
QY 181 KLDELDECKKASSAKORLKASQKGERAFKAWARLVSORFPKAEFAEVSCLVTLDTLK 240
Db 205 KLDVAKERLVAARVQRKSSMQRGERAFKAWARLVSORFPKAEFAEITKATDVTK 264
QY 241 VHTCECHGDLLECCADRADLAKYICENQDSISSKLEKCECKPLEKSHCHIAEYVNDMPA 300
Db 265 INKCECHGDLLECCADRADLAKYICENQDSISSKLEKCECKPLEKSHCHIAEYVNDMPA 324
QY 301 DLPSLAADFVESKDVCKNAEAKDVLGMLFYEYARRHPDYSVLLRLAKTYETTLK 360
Db 325 DLPSLAADFVESKDVCKNAEAKDVLGMLFYEYARRHPDYSVLLRLAKTYETTLK 384
QY 361 CAADPHCYAKVDFEKLVEPQNLKONCELFQOLGEYKFNALLVRYTKVQVST 420
Db 385 CAEGDPPACYGTVLAEFQPLVEEPKLVKTNCELYEKLGEYFQNALVRYTKVQVST 444

QY 422 TLVEVSRNLKGVSKCKHPEAKRMPACADYLSVVLNQLCVLHEKTPVSDRVTKCCTESL 481
DB 447 TLVEAARSLGRVTHCCALPEKRLPCVEDYLSAILNRVLLHEKTPVSEQVTKCCSGK 506
QY 482 VNRPCFSALEVDYTPPKFENAEFTFFHADICTLSEKERQIKKQATLVALVELVKKPKATK 541
DB 507 VERRPCFSALEVDYTPPKFENAEFTFFHADICTLSEKERQIKKQATLVALVELVKKPKATK 566
QY 542 EQLKAVMDFFAAVFEKCKCAKDETCFAEBGKKLVAASQAAL 583
DB 567 EQLKAVMDFFAAVFEKCKCAKDETCFAEBGKKLVAASQAAL 608
RESULT 10
A05139
serum albumin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Jun-1987 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: A05139; I48638
R:Minthetti, P.P.; Law, S.W.; Dugaiczky, A.
Mol. Biol. Evol. 2, 347-358, 1985
A:Title: The rate of molecular evolution of alpha-fetoprotein approaches that of pseudogenes
A:Reference number: A93055; MUID:88216123; PMID:2452956
A:Accession: A05139
A:Molecule type: mRNA
A:Residues: 1-418 <MIN>
A:CROSS-references: GB:M16111; NID:g191764; PIDN:AAA37190.1; PID:g191765
R:Bocaccio, C.; Deschattre, J.; Meunier-Rotival, M.
Gene 88, 181-186, 1990
A:Title: Empty and occupied insertion site of the truncated LINE-1 repeat located in the genome of the mouse
A:Reference number: I48638; MUID:90269606; PMID:1971802
A:Accession: I48638
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 379-453 <BOC>
A:CROSS-references: EMBL:X13060; NID:g52939; PIDN:CAA31458.1; PID:g899334
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; duplication; metal binding; plasma
F:1-104/Domain: serum albumin repeat homology (fragment) <SA1>
F:123-296/Domain: serum albumin repeat homology <SA2>
F:315-453/Domain: serum albumin repeat homology (fragment) <SA3>
Query Match 60.0%; Score 1861; DB 2; Length 453;
Best Local Similarity 72.2%; Pred. No. 8.3e-116;
Matches 327; Conservative 64; Mismatches 62; Indels 0; Gaps 0;

QY 75 CTVATLRETYGEMADCCAKQEPNERCEFLQHKDDNPNLPLRVPRVDMCTAFHDNEET 134
DB 1 CAIPNLRENYGELADCCCTKQEPNERCEFLQHKDDNPNLPLRVPRVDMCTAFHDNEET 60
QY 135 LKLYVEIARRHPYFYFAPELLFFAKRYKAAFTCCCAADKAAACLLPKLDELDEGRASSA 194
DB 61 MGHYLVIEARRHPYFYFAPELLFFAKRYKAAFTCCCAADKAAACLLPKLDELDEGRASSA 120
QY 195 KQRLKCAQKQGERAFKAWAVARLSQRPFAEFAEVSKLVLTDTKVHTVECCCHGDLLECA 254
DB 121 RQRMKSSMQKGERAFKAWAVARLSQRPFAEFAEVSKLVLTDTKVHTVECCCHGDLLECA 180
QY 255 DDRADLAKYICENQDSISSKLECKCEKPLLEKSHCAEVENDEMPADLPSLAADFVESKD 314
DB 181 DRAELAKYICENQATISSKLECKCEKPLLEKSHCAEVENDEMPADLPSLAADFVESKD 240
QY 315 VCKNYAEAKDVFLGMFLYEVARRHPYVSVVLLRLAKTYETTTLEKCCAAADPHECVAKVF 374
DB 241 VCKNYAEAKDVFLGMFLYEVARRHPYVSVVLLRLAKTYETTTLEKCCAAADPHECVAKVF 300
QY 375 DEFKPLVEEPQNTIKONCELFQGLGYKFNALLRYTKVPOVSTPTLVEVSRNLGKVG 434
DB 301 AEFQPLVEEPKLVKNTCDLYELGEGYFQNALVRYTKAPQVSTPTLVEAARNLGRVG 360
QY 435 SKCKKHPKARMPACADYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVARPPCFSALEVD 494
DB 361 TKCTTFEDQRLPCVEDYLSAILNRVLLHEKTPVSEHVTKCCSGSLVRRPCFSALTVD 420

QY 495 ETYVPKEFNAETFFHADICTLSEKERQIKKQT 527
DB 421 ETYVPKEFNAETFFHADICTLPEKEKQIKKQT 453
RESULT 11
ABCHS
serum albumin precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C:Accession: S15571; A05078; A13451
R:Cassady, A.I.; Salkild, C.K.; Baverstock, P.; Wallace, J.C.
submitted to the EMBL Data Library, July 1991
A:Reference number: S15571
A:Accession: S15571
A:Molecule type: mRNA
A:Residues: 1-615 <CAS>
A:CROSS-references: EMBL:X60688; NID:g63747; PIDN:CAA43098.1; PID:g63748
R:Hache, R.J.G.; Wiskocil, R.; Vasa, M.; Roy, R.N.; Lau, P.C.K.; Deeley, R.G.
J. Biol. Chem. 258, 4556-4564, 1983
A:Title: The 5' noncoding and flanking regions of the avian very low density apolipoprotein
A:Reference number: A05078; MUID:83161037; PMID:6187737
A:Accession: A05078
A:Molecule type: DNA
A:Residues: 1-28 <HAC>
A:CROSS-references: GB:V00381; NID:g63038; PIDN:CAA23680.1; PID:g63039
R:Rosen, A.M.; Geller, D.M.
Biochem. Biophys. Res. Commun. 78, 1060-1066, 1977
A:Title: Chicken microsomal albumin: amino terminal sequence of chicken proalbumin.
A:Reference number: A13451; MUID:78019943; PMID:911327
A:Accession: A13451
A:Molecule type: protein
A:Residues: 19-23, M', 25-30 <ROS>
C:Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper
mones (weak bonds with these hormones promote their transfer across the membranes),
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; duplication; metal binding; plasma
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-26/Domain: propeptide #status predicted <PRO>
F:27-613/Product: serum albumin #status predicted <MAT>
F:32-206/Domain: serum albumin repeat homology <SA1>
F:225-398/Domain: serum albumin repeat homology <SA2>
F:417-596/Domain: serum albumin repeat homology <SA3>
F:430/Binding site: copper (HIS) #status predicted
F:80-89,102-118,117-128,152-197,196-205,228-274,273-281,293-307,306-317,344-389,388-3
Query Match 50.2%; Score 1557.5; DB 1; Length 615;
Best Local Similarity 46.7%; Pred. No. 1.4e-95;
Matches 273; Conservative 118; Mismatches 192; Indels 1; Gaps 1;

QY 3 HKSEVAHRPKDLGEEFNFKALVLIATFAQYLOQCPFDHVKLVNEVTEFAKCTVADESANEC 62
DB 30 HKSEIARRNDLKEETFFAKVITFAQYLOQCSYGLSKLVKDVLDAOKCVANEDAPEC 89
QY 63 DKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPNERCEFLQHKDDNPNLPR-LVRAPEVD 121
DB 90 SKPLPSIILDEICQVEKLRDSYGAMADCCSKADPERNECEFLSEKVSQPDVQYQRPASD 149
QY 122 VMCTAFHDNEETPKKYLYEIAARRHPYFYFAPELLFFAKRYKAAFTCCCAADKAAACLLPK 181
DB 150 VICQEQDNRVSPGLGHFIYVARRHPFLYAPALISFAVDPEHALQSCCKESDVGACLDTK 209
QY 182 LDLEDEGRASSAKORLKCASQKQGERAFKAWAVARLSQRPFAEFAEVSKLVLTDTKV 241
DB 210 EIVMRKAGVSVKQYFCILKQFGDRVFAQRLIYLSQKYKPAPFSEVSKFVHDSIGV 269
QY 242 HTCCCHGDLLECAADDRADLAKYICENQDSISSKLECKCEKPLLEKSHCAEVENDEMPAD 301
DB 270 HKCECEDVMECHDDMARWMSNLCSQDDVFSQKIKCCCKEPIVERSQCIWEAEFEDEKPAD 329
QY 302 LPSLAADFVESKDVCNKYAEAKDVFLGMFLYEVARRHPYVSVVLLRLAKTYETTTLEKCC 361
DB 361 TKCTTFEDQRLPCVEDYLSAILNRVLLHEKTPVSEHVTKCCSGSLVRRPCFSALTVD 420

Db 330 LPSLVKEKVEDKVSFEAGHDAFMAEFVVEYSRRHPEFSLIQLIMRIAKGVESLLEKCC 389
 Qy 362 AAADPHECYAKVDFEKLVEEONLIKONCELFQOLGEYKFNQALLVRYTKKVPQVSTP 421
 Db 390 KTDNPAECYANAEOQLNHQIETQDVVNTCDLHHDGEADFLSKILRYTKKMPQVPTD 449
 Qy 422 TLVEVSRNLGVGSKCKHPKAPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCTESL 481
 Db 450 LLLGTGKMTTIGTKCCQLGEDRRMACSEGLSVIHDTCRKQETTPINDNVSCCSQLY 509
 Qy 482 VNRRCFSALEVDETYVPKFNAEFTTFHADICILSEKERQIKKOTALVELVKHKPKATK 541
 Db 510 ANRRCFTAMGVDTKYVPPFNPDMFSEDEKLCSAPAEEREVGQMKLLINLIKRPQMT 569
 Qy 542 EQLKAVMDDFAAVFKCKCKADDKETCFABEGGKLVAAASQAALGL 585
 Db 570 EQIKTIAGFTAMVDKCKQSDINTCFGEAGNLIIVQSRAVLGI 613

RESULT 12
 JC4258
 alpha-fetoprotein precursor - chimpanzee
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 27-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 20-Aug-1999
 C:Accession: JC4258
 R:Nishio, H.; Gibbs, P.E.M.; Minghetti, P.P.; Zielinski, R.; Dugaiczky, A.
 Gene 162, 213-220, 1995
 A:Title: The chimpanzee alpha-fetoprotein-encoding gene shows structural similarity to
 A:Reference number: JC4258; MUID:96032345; PMID:7557431
 A:Accession: JC4258
 A:Molecule type: DNA
 A:Residues: 1-609 <NTS>
 A:Cross-references: GB:U21916; NID:g841311; PIDN:AAA91641.1; PID:g841312
 C:Comment: This protein is a plasma protein produced in the fetal and neonatal liver and
 o similar properties and structure.
 C:Genetics: afp
 A:Gene: afp
 A:Map position: 3p
 A:Introns: 29/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 430/2; 476/3; 551/3
 C:Superfamily: serum albumin; serum albumin repeat homology
 C:Keywords: glycoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-609/Product: alpha-fetoprotein #status predicted <MAT>
 F:29-202/Domain: serum albumin repeat homology <SA1>
 F:221-394/Domain: serum albumin repeat homology <SA2>
 F:413-592/Domain: serum albumin repeat homology <SA3>
 F:42,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.4%; Score 1253.5; DB 2; Length 609;
 Best Local Similarity 40.1%; Pred. NO. 1.9e-75;
 Matches 236; Conservative 115; Mismatches 231; Indels 7; Gaps 3;

Qy 3 HKSE-----VAHRFDLGEENFKALVLAFAQYLOQCFEDHVKLVNVEFPAKTCVADE 57
 Db 22 HNEYGIASILDSYQCTAEINTDLATIFFAQVQEAITYKEVSKVMKDALTAIERKPTGDE 81
 Qy 58 SAENDCKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNP-NLPLVL 116
 Db 82 QSAGCLENQLPAFLBELCREKEILEKYGH-SDCCSQSQSEGRNCFLAHKKPTPASPFPFO 140
 Qy 117 RPEVDVMTAFHDNBEETFLKKLYEITARRHPFYFAPELLFFAKRYKAAAFTECCQAADKAA 176
 Db 141 VPEPVTSCAYEEDRETFMNKFYETIARRHPFLYAPTILLWAARYDKIIPSCCKAENAVE 200
 Qy 177 CLLPKLDELDRGKASSAKQRLKASLQKFGERAFKANAVARLSORFPKAEFAEVSKLVT 236
 Db 201 CFQTKAATVTKELRESSLLNQHACAVMKNFGRTRTFQAITVTLSQKFTKVNTEIQKLVL 260
 Qy 237 DLTQVHTECHGDLLECADRADLAKYICENODSISLKLKCECEKPLEKSKHCAIEVND 296
 Db 261 DVAHVHEHCCRGDVLDCLODGEKIMSYICSQODTUSNKTICECKTTLDERGQCIHAEND 320
 Qy 297 EMPADLPSLAADFVESKDVCKNYAEAKDVLGMLFLEYARRHPDYSVVLRLAKTYETT 356

Db 321 EKPEGLSPNLNRLGDRDFNQFSSEKKNIFLASFVHEYSRRHPQLAVSVILRVAKGYOEL 380
 Qy 357 LEKCCAAADPHECYAKVDFEKLVEEONLIKONCELFQOLGEYKFNQALLVRYTKKVP 416
 Db 381 LEKCFQTEPNLECDQKBEEELQYIQESQALAKRCGLFQKLGYYLQNALVATVKKAP 440
 Qy 417 QVSTPTLVESVRNLGVGSKCKHPKAPCAEDYLSVVLNQLCVLHEKTPVSDRVTKC 476
 Db 441 QLTSSSELMAITRKMAATAATCCQLSEDKLLACGEAADIIGHLCIRHETTPVNFVGVC 500
 Qy 477 CTESLVNRRPFCFALEVDETYVPKFNAEFTTFHADICILSEKERQIKKOTALVELVKHK 536
 Db 501 CTSSVANRRPFCSSLVVDETYVPPAFSDPKFTFHDKDLCAQAGVALQTKQEFLLNLVKOK 560
 Qy 537 PKATKEQLKAVMDDFAAVFKCKCKADDKETCFABEGGKLVAAASQAALGL 585
 Db 561 FOITEEQLEAVTADFSGLEKCKCQEQEVECPAEEGQKLISKYTRALGV 609

RESULT 13
 FPHU
 alpha-fetoprotein precursor [validated] - human
 N:Alternate names: AFP; alpha-1-fetoprotein; alpha-fetoglobulin
 C:Species: Homo sapiens (man)
 C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 08-Dec-2000
 C:Accession: A26624; S37655; A93961; A91497; A23699; A61480; A90624; A90757; A93042;
 R:Gibbs, P.E.M.; Zielinski, R.; Boyd, C.; Dugaiczky, A.
 Biochemistry 26, 1332-1343, 1987
 A:Title: Structure, polymorphism, and novel repeated DNA elements revealed by a compl
 A:Reference number: A26624; MUID:87185438; PMID:2436661
 A:Accession: A26624
 A:Molecule type: DNA
 A:Residues: 1-609 <GTB>
 A:Cross-references: GB:M16110; NID:g773678; PIDN:AA58754.1; PID:g178236
 R:McVey, J.H.; Michaelides, K.; Hansen, L.P.; Ferguson-Smith, M.; Tilghman, S.; Kruml
 Hum. Mol. Genet. 2, 379-384, 1993
 A:Title: A G->A substitution in an HNF I binding site in the human alpha-fetoprotein
 A:Reference number: S37655; MUID:93278385; PMID:7684942
 A:Accession: S37655
 A:Molecule type: DNA
 A:Residues: 1-28 <MCV>
 A:Cross-references: EMBL:Z19532; NID:g28527; PIDN:CAA79592.1; PID:g28528
 A:Note: The authors translated the codon TAT for residue 26 as Thr
 R:Morinaga, T.; Sakai, M.; Wegmann, T.G.; Tamaoki, T.
 Proc. Natl. Acad. Sci. U.S.A. 80, 4604-4608, 1983
 A:Title: Primary structures of human alpha-fetoprotein and its mRNA.
 A:Reference number: A93961; MUID:83273664; PMID:6192439
 A:Accession: A93961
 A:Molecule type: mRNA
 A:Residues: 1-609 <MOR>
 A:Cross-references: GB:J00077; NID:g311348; PIDN:CAA24758.1; PID:g31351
 R:Beattie, W.G.; Dugaiczky, A.
 Gene 20, 415-422, 1982
 A:Title: Structure and evolution of human alpha-fetoprotein deduced from partial sequ
 A:Reference number: A91497; MUID:83158778; PMID:6187626
 A:Accession: A91497
 A:Molecule type: mRNA
 A:Residues: 429-556 <BEA>
 A:Cross-references: GB:J00076
 R:Pucci, P.; Siciliano, R.; Malorni, A.; Marino, G.; Tecce, M.F.; Ceccarini, C.; Terr
 Biochemistry 30, 5061-5066, 1991
 A:Title: Human alpha-fetoprotein primary structure: a mass spectrometric study.
 A:Reference number: A23699; MUID:91242409; PMID:1709810
 A:Accession: A23699
 A:Molecule type: protein
 A:Residues: 19-45;60-97;102-107;122-184;187-249;255-489;507-609 <PUC>
 R:Tecce, M.F.; Terrana, B.; Giuliani, M.M.; Ceccarini, C.
 J. Nucl. Med. Allied Sci. 34, 213-216, 1990
 A:Title: Characterization of in vitro expressed human alpha-fetoprotein as highly rep
 A:Reference number: A61480; MUID:91225826; PMID:1709209
 A:Accession: A61480
 A:Molecule type: protein

Db 141 VPEPVTSEAEVEDRETFMNFYIARRHPFLYAPTILLWAARYDKIIPSCCKAENAVE 200
Qy 177 CLLPKLDLDRDGBKASSAKQRLKASLOKFGGERAFKANAVARLSORFEPKAEFAEYKSLVT 236
Db 201 CFQTKAAVTKELRESSLLNQHACAVMKNFGTRTQAITVTKLSORFTKVNTEIQKLVL 260
Qy 237 DUTKVHTECCGGDLLECDRADLAKYICENODSISKLKECEKPLLEKSHCIAEVEND 296
Db 261 DVAVHVEHCCRGDVLCDLQDGBEKINSYCSQODTSLNKITECKLTTLERGQCIHAEND 320
Qy 297 ENPADLPSLAADFVESKQCKNYAAKADVFLGFMFLYEVARRHPDYSVLLLLAKTYETT 356
Db 321 EKPEGLSPNLNRLFGDRDNFQSSGEKNITFLASFVHEYSRRHPQLAVSVILFVAKGYOEL 380
Qy 357 LEKCCAAADPHCYAKVDFEKFPLVEEPNLIKONCELFEOELGEYKFNALLVRYTKVP 416
Db 381 LEKCFQTNLENQCQDKGEEELQKYIQESQALAKRSCGLFQKLGYYLQNAFLVATYTKAP 440
Qy 417 QVSTPLVSVRNKGVSKCKKHPKAEKMPCAEDYLSVNLQCLVHLKEKTPVSDRVTKC 476
Db 441 QLTSSELAITRKMAATAATCCQSEDKLLACGEGAADIIGHLCIRHEMTPVNPVGQC 500
Qy 477 CTESLVNRRPFSALEVDETYVPKEFNAETFTFHADICTLSKEKQIKQTALVELVKHK 536
Db 501 CTSSYANRRPFSLLVVDETYVPPAFSDDKETFHKDLQCAQGVALQTMKQEFNLNVRKQK 560
Qy 537 PKATKEQLKAVMDFAAEVEKCKADDKETCTFAEKGKLVAAASQAALGL 585
Db 561 POITEEQLETVIADPSGLLEKCCQGEQEVCFAEQGLSKIRTLALGV 609

RESULT 15
ABXL72

74K albumin precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C:Accession: B41682; S02693; A05288
R:Moskatis, J.E.; Sargent, T.D.; Smith Jr., L.H.; Pastori, R.L.; Schoenberg, D.R.
Mol. Endocrinol. 3, 464-473, 1989
A:Title: Xenopus laevis serum albumin: sequence of the complementary deoxyribonucleic acid during development.
A:Reference number: A41682; MUID:89313788; PMID:2747653
A:Accession: B41682
A:Residues: 3-607 <MOS>
A:Molecule type: mRNA
A:Cross-references: GB:W21442; NID:g213930; PIDN:AA49637.1; PID:g213931
R:Schorpp, M.; Doebebling, U.; Wagner, U.; Ryffel, G.U.
J. Mol. Biol. 199, 83-93, 1988
A:Title: 5'-flanking and 5'-proximal exon regions of the two Xenopus albumin genes. Deleted exon 5' is present in the 5'-flanking region of the 5'-proximal exon.
A:Reference number: S02692; MUID:88172470; PMID:2451026
A:Accession: S02693
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Cross-references: EMBL:Z26826
R:Wolfe, A.P.; Glover, J.F.; Martin, S.C.; Tenniswood, M.P.R.; Williams, J.L.; Tata, J.
Eur. J. Biochem. 146, 489-496, 1985
A:Title: Deinduction of transcription of Xenopus 74-kDa albumin genes and destabilization of the 5'-proximal exon.
A:Reference number: A05288; MUID:85126974; PMID:3971963
A:Accession: A05288
A:Molecule type: mRNA
A:Residues: 459-502, 'L' 504-557 <WOL>
A:Cross-references: GB:W28276
A:Note: The authors translated the codon TAT for residue 63 as Thr
C:Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, mones (weak bonds with these hormones promote their transfer across the membranes), thyroglobulin, and retinol.
C:Genetics:
A:Introns: 27/1
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; duplication; glycoprotein; metal binding; plasma
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-24/Domain: propeptide #status predicted <PRO>

F:25-607/Product: 74K serum albumin #status predicted <MAT>
F:320-201/Domain: serum albumin repeat homology <SA1>
F:220-393/Domain: serum albumin repeat homology <SA2>
F:412-591/Domain: serum albumin repeat homology <SA3>
F:30/Binding site: copper (His) #status predicted
F:80-88,101-117,116-127,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-384
F:256/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.8%; Score 1205; DB 1; Length 607;
Best Local Similarity 39.3%; Pred No. 3e-72;
Matches 227; Conservative 108; Mismatches 239; Indels 4; Gaps 2;

Qy 3 HKSEVAHFRKDLGEENFKALVLIAPFAQYLQCCPFEDHVKLVNEVTEFAKTCAVDESAENC 62
Db 30 HHKHIADVYALTERTFKGLTIAIVSONLQKCSLELSKLVNEINDEFAKSCINDKTPC-C 88
Qy 63 DKSLLHTLFGDKLCTVATLRETTYGEMADCCAKQEPERNECFLOHKDDNPNLPLRVREPDV 122
Db 89 EKPVGTLFFDKLCAADPAVGVNVEYSEKCAQKQDPERAQCFAHRDHEHT---SIKPEPEE 145
Qy 123 MCTAFHDNEETFLKKVLYEIAARRHPVYAPPELLFTAKRYKAAFTCCCAADAAACULLPKL 182
Db 146 TCKLLKEHPDDLLSAFIIHEARNHPDLYPPAVLALTQYTKLAEHCEDEEDKEKCFSEAM 205
Qy 183 DELRDEGKASSAKQRLKASLOKFGGERAFKANAVARLSORFEPKAEFAEYKSLVTDLTKVH 242
Db 206 KOLMKQSHSIEDKQHHFCWILONFPEKVLKALNARVSHRYPKAEKLAHNFTTEVTHFI 265
Qy 243 TCCCHGDLLECDRADLAKYICENODSISKLKECEKPLLEKSHCIAEVENDEMPADL 302
Db 266 KDCCHDDMFECMTERLELTHCTQHKDELSSKLEKCCNIPLLERTYCIIVTLENDVPAEL 325
Qy 303 PSLAADFVESKQCKNYAAKADVFLGFMFLYEVARRHPDYSVLLLLRLAKTYETTLKCCA 362
Db 326 SPTITEFTEDPHVCYKAEENNEVFLGRYLHAVSRKHQELSEDFLOSAKEYESLNNKCK 385
Qy 363 AADPHECYAKVDFEKFPLVEEPNLIKONCELFEOELGEYKFNALLVRYTKVPQVSTPT 422
Db 386 TDNPPECYKOGADREMNEAKERFAVLKQNCIDLHEHGEYLFENELLIRYTKMPQVSD 445
Qy 423 LVEVSRNLGKGVSKCKKHPKAEKMPCAEDYLSVNLQCLVHLKEKTPVSDRVTKCCTESLV 482
Db 446 LIGIAHQADIGEHCACAVPENQMPCAEGDLTILIGKMCERQKKTFINNHVAHCCTDSYS 505
Qy 483 NRPFCFSALEVDETYVPKEFNAETFTFHADICTLSKEKQIKQTALVELVKHKPRATKE 542
Db 506 GMRSCFTALGPPDEDYVPPVTDTHFDKICTADKEKQHKQKFLVKLIVSPKLEKN 565
Qy 543 QLKAVMDFAAEVEKCKADDKETCTFAEKGKLVAAASQ 580
Db 566 HIDECSAEFLKMWQKCCCTADEHQPCFDTTEKPVLEHCQ 603

Search completed: April 24, 2003, 07:23:12
Job time : 24 secs

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GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: April 24, 2003, 07:22:18 ; Search time 14 Seconds
(without alignments)
1733.118 Million cell updates/sec

Title: us-09-833-111-18

Perfect score: 3103

Sequence: 1 DAHSEVAHFKDLGENFK.....TCFAEGCKLVASQAALGL 585

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3103	100.0	609	1	ALBU_HUMAN
2	2942	94.8	600	1	ALBU_MACMU
3	2620	84.4	608	1	ALBU_FELCA
4	2562	82.6	608	1	ALBU_CANFA
5	2475.5	79.8	607	1	ALBU_HORSE
6	2450.5	79.0	607	1	ALBU_BOVIN
7	2446	78.8	608	1	ALBU_RABIT
8	2432.5	78.4	607	1	ALBU_SHEEP
9	2426	78.2	608	1	ALBU_RAT
10	2411.5	77.7	605	1	ALBU_PIG
11	2387	76.9	609	1	ALBU_MERUN
12	2378	76.6	608	1	ALBU_MOUSE
13	1557.5	50.2	615	1	ALBU_CHICK
14	1253.5	40.4	609	1	FETA_PANTR
15	1249.5	40.3	609	1	FETA_HUMAN
16	1242.5	40.0	609	1	FETA_GORGO
17	1205	38.8	607	1	ALBU2_XENLA
18	1200	38.7	609	1	FETA_HORSE
19	1164.5	37.5	605	1	ALBL_XENLA
20	1084	34.9	605	1	FETA_MOUSE
21	1067	34.4	611	1	FETA_RAT
22	1055	34.0	599	1	AFAM_HUMAN
23	944	30.4	611	1	AFAM_MOUSE
24	928	29.9	608	1	AFAM_RAT
25	747.5	24.1	608	1	ALBL_SALSA
26	742.5	23.9	608	1	ALBL_SALSA
27	699	22.5	382	1	ALBU_RANCA
28	440.5	14.2	1423	1	ALBU_PETMA
29	386	12.4	474	1	VTDB_HUMAN
30	381	12.3	476	1	VTDB_RAT
31	378	12.2	476	1	VTDB_RABIT
32	372	12.0	472	1	VTDB_MOUSE
33	133.5	4.3	1391	1	MST2_DROHY

RESULT 1

ID	ALBU_HUMAN	STANDARD	PRT	609 AA
AC	P02768; Q13140; Q9UJ20; Q9UHS3; Q9PL17; Q9P157; Q9S574;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Serum albumin precursor.			
GN	ALB.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=86196112; PubMed=3009475;			
RX	Minghetti P.P., Ruffner D.E., Kuang W.J., Dennison O.E., Hawkins J.W.,			
RA	Beattie W.G., Dugaiczak A.;			
RT	"Molecular structure of the human albumin gene is revealed by			
RT	nucleotide sequence within q11-22 of chromosome 4.";			
RL	J. Biol. Chem. 261:6747-6757(1986).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82081882; PubMed=6171778;			
RA	Lawn R.M., Adelman J., Bock S.C., Franke A.E., Houck C.M.,			
RA	Najarian R.C., Seeburg P.H., Wion K.L.;			
RT	"The sequence of human serum albumin cDNA and its expression in E.			
RT	coli.";			
RL	Nucleic Acids Res. 9:6103-6114(1981).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82105994; PubMed=6275391;			
RA	Dugaiczak A., Law S.W., Dennison O.E.;			
RT	"Nucleotide sequence and the encoded amino acids of human serum			
RT	albumin mRNA.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:71-75(1982).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Liver;			
PC	Yang S., Zhang R.A., Qi Z.W., Yuan Z.Y.;			
RA	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Fetal liver;			
RA	Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,			
RA	He F.;			
RT	"Functional prediction of the coding sequences of 79 new genes deduced			
RT	by analysis of cDNA clones from human fetal liver.";			
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE OF 25-609.			
RX	MEDLINE=76187907; PubMed=1225573;			
RA	Meloun B., Moravsek I., Kostka V.;			
RT	"Complete amino acid sequence of human serum albumin.";			
RL	FEBS Lett. 58:134-137(1975).			
RN	[7]			

ALIGNMENTS

RP SEQUENCE OF 25-609.
RA Brown J.R., Shockley P., Behrens P.Q.;
RL (in) Bing D.H. (eds.);
RL The chemistry and physiology of the human plasma proteins, pp.23-40,
RL Pergamon Press, New York (1979).
RN [8]
RP SEQUENCE OF 1-455 FROM N.A.
RC TISSUE=Liver;
RA Menaya J., Parrilla R., Ayuso M.S.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [9]
RP PARTIAL SEQUENCE FROM N.A. (PRO2619/PRO2044/PRO1708/PRO2675).
RC TISSUE=Fetal liver;
RA Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Y.,
RA Xu W., Gao F., Liu M., He F., Zhang Y., Ouyang S., Luo L.;
RT "Functional prediction of the coding sequences of 121 new genes
RT deduced by analysis of cDNA clones from human fetal liver";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE OF 1-26 FROM N.A.
RC TISSUE=Liver;
RA Urano Y., Watanabe K., Sakai M., Tamaoki T.;
RL "The human albumin gene. Characterization of the 5' and 3' flanking
RT regions and the polymorphic gene transcripts.";
RL J. Biol. Chem. 261:3244-3251(1986).
RN [11]
RP SEQUENCE OF 222-229.
RC TISSUE=Liver;
RA Walker J.E.;
RL MEDLINE=76257808; PubMed=955075;
RP SEQUENCE OF 25-44 AND 480-499.
RC TISSUE=Heart;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.";
RL Electrophoresis 15:1459-1465(1994).
RN [13]
RP SEQUENCE OF 409-609 FROM N.A.
RC TISSUE=Skeletal muscle;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [14]
RP DISULFIDE BONDS.
RA Saber M.A., Stockbauer P., Moravsek L., Meloun B.;
RT "Disulfide bonds in human serum albumin";
RL Collect. Czech. Chem. Commun. 42:564-579(1977).
RN [15]
RP BILIRUBIN-BINDING SITE.
RA Jacobson C.;
RT "Lysine residue 240 of human serum albumin is involved in high-
RT affinity binding of bilirubin";
RL Biochem. J. 171:453-459(1978).
RN [16]
RP VARIANT CANTERBURY.
RA Brennan S.O.;
RL MEDLINE=87157744; PubMed=3828358;
RT "Albumin Canterbury (313 Lys->Asn). A point mutation in the second
RT domain of serum albumin";
RL Biochim. Biophys. Acta 912:191-197(1987).
RN [17]
RP VARIANTS NAG-2 AND NAG-3.
RA Takahashi N., Takahashi Y., Isobe T., Putnam F.W., Fujita M.,
RA Satoh C., Neel J.V.;
RT "Amino acid substitutions in inherited albumin variants from
RT Amerindian and Japanese populations";
RL Proc. Natl. Acad. Sci. U.S.A. 84:8001-8005(1987).
RN [18]

RP VARIANTS NAG-1, HIR-1, HIR-2 AND TOCHIGI.
RX MEDLINE=89345611; PubMed=2762316;
RA Arai K., Madison J., Huss K., Ishioke N., Satoh C., Fujita M.,
RA Neel J.V., Sakurabayashi I., Putnam F.W.;
RT "Point substitutions in Japanese albumins";
RL Proc. Natl. Acad. Sci. U.S.A. 86:6092-6096(1989).
RN [19]
RP VARIANTS MANAUS; OSAKA; NAGOYA; FUKUOKA; HONOLULU AND NEW-GUINEA.
RX MEDLINE=90115905; PubMed=2404284;
RA Arai K., Madison J., Shimizu A., Putnam F.W.;
RT "Point substitutions in albumin genetic variants from Asia.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:497-501(1990).
RN [20]
RP VARIANT REDHILL.
RX MEDLINE=90115852; PubMed=2104980;
RA Brennan S.O., Myles T., Peach R.J., Donaldson D., George P.M.;
RT "Human Redhill (-1 Arg, 320 Ala->Thr): a glycoprotein variant of
RT albumin serum albumin whose precursor has an aberrant signal peptidase
RT cleavage site";
RL Proc. Natl. Acad. Sci. U.S.A. 87:26-30(1990).
RN [21]
RP VARIANTS TORINO; VARESE AND VIBO VALENTIA.
RX MEDLINE=91062352; PubMed=2247440;
RA Galliano M., Minchiotti L., Porta F., Rossi A., Ferri G., Madison J.,
RA Watkins S., Putnam F.W.;
RT "Mutations in genetic variants of human serum albumin found in
RT Italy";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8721-8725(1990).
RN [22]
RP VARIANT VENEZIA.
RX MEDLINE=91296740; PubMed=2068071;
RA Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M.,
RA Minchiotti L., Putnam F.W.;
RT "A donor splice mutation and a single-base deletion produce two
RT carboxyl-terminal variants of human serum albumin";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5959-5963(1991).
RN [23]
RP VARIANTS IOWA CITY AND KOMAGOME.
RX MEDLINE=92052189; PubMed=1946412;
RA Madison J., Arai K., Feld R.D., Kyle R.A., Watkins S., Davis E.,
RA Matsuda Y., Amaki I., Putnam F.W.;
RT "Genetic variants of serum albumin in Americans and Japanese";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9853-9857(1991).
RN [24]
RP VARIANT CASEBROOK.
RX MEDLINE=91316157; PubMed=1859851;
RA Peach R.J., Brennan S.O.;
RT "Structural characterization of a glycoprotein variant of human serum
RT albumin: albumin Casebrook (494 Asp->Asn)";
RL Biochim. Biophys. Acta 1097:49-54(1991).
RN [25]
RP VARIANTS SONDRIO AND PARIS-2.
RX MEDLINE=92190239; PubMed=1347703;
RA Minchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H.,
RA Rochu D., Porta F.;
RT "Two albumins with identical electrophoretic mobility are produced
RT by differently charged amino acid substitutions";
RL Biochim. Biophys. Acta 1119:232-238(1992).
RN [26]
RP VARIANTS MALMO.
RX MEDLINE=92390419; PubMed=1518850;
RA Carlson J., Sakamoto Y., Laurell C.-B., Madison J., Watkins S.,
RA Putnam F.W.;
RT "Alloalbuminemia in Sweden: structural study and phenotypic
RT distribution of nine albumin variants";
RL Proc. Natl. Acad. Sci. U.S.A. 89:8225-8229(1992).
RN [27]
RP VARIANT HERBORN.
RX MEDLINE=93292504; PubMed=8513793;
RA Minchiotti L., Galliano M., Zapponi M.C., Tenni R.;
RT "The structural characterization and bilirubin-binding properties of
RT albumin Herborn, a [Lys240->Glu] albumin mutant";
RL Eur. J. Biochem. 214:437-444(1993).

```

Query Match      100.0%; Score 3103; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 2.7e-195;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHSEVAHREFKDLGEENFKALVLIATFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 60
Db 25 DAHSEVAHREFKDLGEENFKALVLIATFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 84
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPERNECFLOHKDDNPPLRLVRPEV 120
Db 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPERNECFLOHKDDNPPLRLVRPEV 144
Qy 121 DVMCTAFHDNEETFLKYLVIETARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
Db 145 DVMCTAFHDNEETFLKYLVIETARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 204
Qy 181 KLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSCLVTDLT 240
Db 205 KLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSCLVTDLT 264
Qy 241 VHTCCCHGDLLECADRADLAKYICENODSISSKLECCCEKPILEKSHCIAEVENDEMPA 300
Db 265 VHTCCCHGDLLECADRADLAKYICENODSISSKLECCCEKPILEKSHCIAEVENDEMPA 324
Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFGLGMFLYEXARRHPDYSVVLLRLAKTYETTLK 360
Db 325 DLPSLAADFVESKDVCKNYAEAKDVFGLGMFLYEXARRHPDYSVVLLRLAKTYETTLK 384
Qy 361 CAADPHECYAKVDFEKPFLVEEPONLIKONCELFQOLGEYKFQNALVRYTKVPQVST 420
Db 385 CAADPHECYAKVDFEKPFLVEEPONLIKONCELFQOLGEYKFQNALVRYTKVPQVST 444
Qy 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHKTVPVSRVTKCCTES 480
Db 445 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHKTVPVSRVTKCCTES 504
Qy 481 LVNRRPFCFSALEVDVETVPVREFNAETTFHADICTLSEKERQIKKQALVELVLRHKPKAT 540
Db 505 LVNRRPFCFSALEVDVETVPVREFNAETTFHADICTLSEKERQIKKQALVELVLRHKPKAT 564
Qy 541 KEQLKAVMDPFAAEVCKCKADKCTCFABEGKKLVAAASQAALGL 585
Db 565 KEQLKAVMDPFAAEVCKCKADKCTCFABEGKKLVAAASQAALGL 609

RESULT 2
ALBU_MACMU STANDARD; PRT; 600 AA.
AC Q28522;
AT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor (Fragment).
GN ALB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93211971; PubMed=8460152;
RA Watkins S.A., Sakamoto Y., Madison J.M., Davis E.M., Smith D.G.,
RA Dwulet J., Putnam F.W.;
RT "cDNA and protein sequence of polymorphic macaque albumins that differ
RT in bilirubin binding.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2409-2413(1993).
CC -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -!- SUBCELLULAR LOCATION: Secreted.

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CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
CC -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M90463; AAA36906.1; -
CC HSP; P02768; 1E7B.
CC InterPro: IPR000264; Serum_albumin.
CC Pfam: PF00273; transport_prot; 3.
CC ProDom: PD002486; Serum_albumin; 1.
CC SMART: SM00103; ALBUMIN; 3.
CC PROSITE: PS00212; ALBUMIN; 3.
CC Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
CC Copper.
CC -----
CC 1 1
CC SIGNAL <1 10 BY SIMILARITY.
CC PROPEP 11 16 BY SIMILARITY.
CC CHAIN 17 600 SERUM ALBUMIN.
CC DOMAIN 17 197 ALBUMIN 1.
CC DOMAIN 204 389 ALBUMIN 2.
CC DOMAIN 396 587 ALBUMIN 3.
CC METAL 19 19 COPPER (BY SIMILARITY).
CC BINDING 256 256 BILIRUBIN (POTENTIAL).
CC DISULFID 61 78 BY SIMILARITY.
CC DISULFID 91 107 BY SIMILARITY.
CC DISULFID 106 117 BY SIMILARITY.
CC DISULFID 140 185 BY SIMILARITY.
CC DISULFID 184 193 BY SIMILARITY.
CC DISULFID 216 262 BY SIMILARITY.
CC DISULFID 261 269 BY SIMILARITY.
CC DISULFID 281 295 BY SIMILARITY.
CC DISULFID 294 305 BY SIMILARITY.
CC DISULFID 332 377 BY SIMILARITY.
CC DISULFID 376 385 BY SIMILARITY.
CC DISULFID 408 454 BY SIMILARITY.
CC DISULFID 453 464 BY SIMILARITY.
CC DISULFID 477 493 BY SIMILARITY.
CC DISULFID 492 503 BY SIMILARITY.
CC DISULFID 530 575 BY SIMILARITY.
CC DISULFID 574 583 BY SIMILARITY.
CC SEQUENCE 600 AA; 67880 MW; E45C871A670E740B CRC64;
Query Match 94.8%; Score 2942; DB 1; Length 600;
Best Local Similarity 93.5%; Pred. No. 8.3e-185;
Matches 545; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DAHSEVAHREFKDLGEENFKALVLIATFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 60
Db 17 DTHKSEVAHREFKDLGEENFKALVLIATFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 76
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPERNECFLOHKDDNPPLRLVRPEV 120
Db 77 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPERNECFLOHKDDNPPLRLVRPEV 136
Qy 121 DVMCTAFHDNEETFLKYLVIETARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
Db 137 DVMCTAFHDNEETFLKYLVIETARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 196
Qy 181 KLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSCLVTDLT 240
Db 197 KLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSCLVTDLT 256
Qy 241 VHTCCCHGDLLECADRADLAKYICENODSISSKLECCCEKPILEKSHCIAEVENDEMPA 300
Db 257 VHTCCCHGDLLECADRADLAKYICENODSISSKLECCCEKPILEKSHCIAEVENDEMPA 316

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QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHPDYSVVLLRLAKTYETTLK 360
 Db 317 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHPDYSVVLLRLAKTYETTLK 376
 QY 361 CAADPHCEYAKVDFEKPPLVEBPQNLKONCELFQOLGEYKFNALLVRYTKVPOVST 420
 Db 377 CAADPHCEYAKVDFEKPPLVEBPQNLKONCELFQOLGEYKFNALLVRYTKVPOVST 436
 QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHKTPTVSDRYTKCCTES 480
 Db 437 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHKTPTVSEKVTKCCTES 496
 QY 481 LVNRRPFCFSALEVDYVVPKFEAFNAETFTPHADICTLSEKERQIKKOTALVELVKKHPRKAT 540
 Db 497 LVNRRPFCFSALEVDYVVPKFEAFNAETFTPHADICTLSEKERQIKKOTALVELVKKHPRKAT 556
 QY 541 KEOLKAVMDFAAFVEKCKKADDEKTCFADEGKGLVNAASQAAL 583
 Db 557 KEOLKAVMDFAAFVEKCKKADDEKTCFADEGKGLVNAASQAAL 599

RESULT 3.

ALBU_FELCA STANDARD; PRT; 608 AA.
 AC P49064;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Serum albumin precursor (Allergen Fel d 2).
 GN ALB.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96194824; PubMed=8647469;
 RA Hilger C., Grigioni F., Kohnen M., Hentges F.;
 RT "Sequence of the gene encoding cat (Felis domesticus) serum albumin.";
 RL Gene 169:295-296(1996).
 CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
 CC BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
 CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
 CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.

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 CC -----

DR EMBL: X84842; CAA59279.1;
 DR HSP: P02768; 1E7B.
 DR InterPro: IPR000264; Serum_albumin.
 DR Pfam: PF00273; transport_prot; 3.
 DR PRINTS: PR00802; SERUMALBUMIN.
 DR ProDom: PD002486; Serum_albumin; 1.
 DR SMART: SM00103; ALBUMIN; 3.
 DR PROSITE: PS00212; ALBUMIN; 3.
 KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
 KW Copper; Allergen.
 FT SIGNAL 1 18 BY SIMILARITY.
 FT PROPEP 19 24 BY SIMILARITY.
 FT CHAIN 25 608 SERUM ALBUMIN.
 FT DOMAIN 25 205 ALBUMIN 1.
 FT DOMAIN 212 397 ALBUMIN 2.
 FT DOMAIN 404 595 ALBUMIN 3.

FT METAL 27 27 COPPER.
 FT DISULFID 77 86 BY SIMILARITY.
 FT DISULFID 99 115 BY SIMILARITY.
 FT DISULFID 114 125 BY SIMILARITY.
 FT DISULFID 148 193 BY SIMILARITY.
 FT DISULFID 192 201 BY SIMILARITY.
 FT DISULFID 224 270 BY SIMILARITY.
 FT DISULFID 269 277 BY SIMILARITY.
 FT DISULFID 289 303 BY SIMILARITY.
 FT DISULFID 302 313 BY SIMILARITY.
 FT DISULFID 340 385 BY SIMILARITY.
 FT DISULFID 384 393 BY SIMILARITY.
 FT DISULFID 416 462 BY SIMILARITY.
 FT DISULFID 461 472 BY SIMILARITY.
 FT DISULFID 485 501 BY SIMILARITY.
 FT DISULFID 500 511 BY SIMILARITY.
 FT DISULFID 538 583 BY SIMILARITY.
 FT DISULFID 582 591 BY SIMILARITY.
 SQ SEQUENCE 608 AA; 68659 MW; 07E629CAC3F60B5F CRC64;

Query Match 84.4%; Score 2620; DB 1; Length 608;

Best Local Similarity 82.0%; Pred. No. 8 4e-164;

Matches 478; Conservative 52; Mismatches 53; Indels 0; Gaps 0;

QY 1 DAHKEVAHFRKDLGBENFKALVLIAPAOYLQOCPEFDHVKLVNVEYFAKTCVADSAE 60
 Db 25 EAHQSEIAHFRNDLGBEHPRLVLFVAFSOLQOCPEFDHVKLVNVEYFAKTCVADSAE 84
 QY 61 NCDKSLHTLFGDKLCIVATLRETYGEMADCCAKQEBERNECFLOHKDDNPNLRLVPEV 120
 Db 85 NCKSLHLLGDKLCIVASLRDKYGMADCCCKEPEERNECFLOHKDDNPNLRLVPEV 144
 QY 121 DVNCTAFHNDNEETFLKYLVEIARRHPYFYAPPELLFYFAKRYKAAFTCCOAAAKAACLTP 180
 Db 145 DAMCTAFHNEQRFGLKYLVEIARRHPYFYAPPELLFYFAKRYKAAFTCCOAAAKAACLTP 204
 QY 181 KLDELDECKKASSAKORLKCASLQKFGERAFAKAWAVARLSORPKAEFAEVSKLVTDLT 240
 Db 205 KVDALREKVLASSAKERLKCASLQKFGERAFAKAWAVARLSORPKAEFAEVSKLVTDLT 264
 QY 241 VHTCECHGDLLECADRADLAKYICENQDSISSKKECCCKPILLESKSHCTAEVENDMPA 300
 Db 265 IHKECCCHGDLLECADRADLAKYICENQDSISTKLKCECCGKPVLEKSHCISEVERDELPA 324
 QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHPDYSVVLLRLAKTYETTLK 360
 Db 325 DLPLAVDFVEDKEVCKNYEAKDVLGMLFYEARHPDYSVVLLRLAKTYETTLK 384
 QY 361 CAADPHCEYAKVDFEKPPLVEBPQNLKONCELFQOLGEYKFNALLVRYTKVPOVST 420
 Db 385 CATDDPPACVAHVDFEKPPLVEBPQNLKONCELFQOLGEYKFNALLVRYTKVPOVST 444
 QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHKTPTVSDRYTKCCTES 480
 Db 445 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHKTPTVSDRYTKCCTES 504
 QY 481 LVNRRPFCFSALEVDYVVPKFEAFNAETFTPHADICTLSEKERQIKKOTALVELVKKHPRKAT 540
 Db 505 LVNRRPFCFSALEVDYVVPKFEAFNAETFTPHADICTLSEKERQIKKOTALVELVKKHPRKAT 564

RESULT 4

ALBU_CANFA STANDARD; PRT; 608 AA.
 ID ALBU_CANFA
 AC P49822; 077705; Q9TS24;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Serum albumin precursor (Allergen Can f 3).

GN ALB.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Beagle; TISSUE=Liver;
RA Hilger C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20148667; PubMed=1069848;
RA Pandjaitan B., Swoboda I., Brandesky-Pichler F., Rumpold H.,
RA Valenta R., Spitzauer S.;
RT "Escherichia coli expression and purification of recombinant dog
RT albumin, a cross-reactive animal allergen.";
RL J. Allergy Clin. Immunol. 105:279-285(2000).
RN [3]
RP SEQUENCE OF 25-48.
RX MEDLINE=75011422; PubMed=4414013;
RA Dixon J.W., Sarkar B.;
RT "Isolation, amino acid sequence and copper(II)-binding properties of
RT peptide (1-24) of dog serum albumin.";
RL J. Biol. Chem. 249:5872-5877(1974).
RN [4]
RP SEQUENCE OF 25-38.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
RN [5]
RP SEQUENCE OF 215-478 FROM N.A.
RC TISSUE=Salivary gland;
RX MEDLINE=94201492; PubMed=7512102;
RA Spitzauer S., Schweizer C., Sperr W.R., Pandjaitan B., Valent P.,
RA Muehl S., Ebner C., Scheiner O., Kraft D., Rumpold H.;
RT "Molecular characterization of dog albumin as a cross-reactive
RT allergen.";
RL J. Allergy Clin. Immunol. 93:614-627(1994).
CC -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC BINDING CAPACITY FOR WATER, CA⁺⁺, NA⁺, K⁺, FATTY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AJ133489; CAB64867.1; -;
CC EMBL; Y17737; CAA76841.1; -;
CC EMBL; S72946; AAB30434.1; -;
CC PIR; S29749; S29749.
CC HSP; P02768; 1E7B.
CC HSC-2DPAGE; P49822; DOG.
CC InterPro; IPR000264; Serum_albumin.
CC Pfam; PF00273; transport_prot; 3.
CC PRINTS; P00802; SERUMALBUMIN.
CC ProDom; PD002486; Serum_albumin; 1.
CC SMART; SM00103; ALBUMIN; 3.
CC PROSITE; PS00212; ALBUMIN; 3.
KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;

Copper; Allergen. 18
FT SIGNAL 1
FT PROPEP 19
FT CHAIN 24
FT DOMAIN 25
FT DOMAIN 25
FT DOMAIN 212
FT DOMAIN 404
FT METAL 27
FT DISULFID 77
FT DISULFID 77
FT DISULFID 99
FT DISULFID 114
FT DISULFID 148
FT DISULFID 192
FT DISULFID 224
FT DISULFID 269
FT DISULFID 289
FT DISULFID 302
FT DISULFID 340
FT DISULFID 384
FT DISULFID 416
FT DISULFID 461
FT DISULFID 485
FT DISULFID 500
FT DISULFID 538
FT DISULFID 582
FT CONFLICT 1
FT CONFLICT 146
FT CONFLICT 206
FT CONFLICT 349
FT CONFLICT 359
FT CONFLICT 448
FT CONFLICT 474
SQ SEQUENCE 608 AA; 68606 MW; 3CFLC8FF7DD8FC06 CRC64;
Query Match 82.6%; Score 2562; DB 1; Length 608;
Best Local Similarity 79.8%; Pred. No. 5,1e-160;
Matches 465; Conservative 57; Mismatches 61; Indels 0; Gaps 0;
QY 1 DAHSEVAVRFDLGEENFKALVLIAPAOYLQCCPEHDHVKLVNEVTEFAKTQVADESA 60
DB 25 EAYKSEIARHNDLGEHFRGLVAVFSQYLQCCPEHDHVKLAKETEFKAKAABESGA 84
QY 61 NCDKSLHTLFGDKLCTVATIRETYGEMADCCAKQEPERNECFQHKDDNPNLRLVRPEV 120
DB 85 NCDKSLHTLFGDKLCTVATIRETYGEMADCCAKQEPERNECFQHKDDNPNLRLVRPEV 144
QY 121 DVNCTAFHDNEETFLKKYLYETARRHPYFAPPELLFFAKRYKAAFTCCOAAADKACLLP 180
DB 145 DALCAAFQDNEQLFLGKLYETARRHPYFAPPELLFYAQQYKGVFAECCQAADKACLGP 204
QY 181 KLDELDEGKASSAKORLKCASLOKGEFRAFAKAWARLSQREPKAEFVSKLVTDLT 240
DB 205 KTEALREKVLSSAKERFKCASLQKDFGDFRAKAWARLSQREPKADFAEISKVVTDLT 264
QY 241 VITECHGDLLECCADRADLAKYICENQDSISSKLECECKPLEKSHCIAEVENDEMPA 300
DB 265 VHKCECHGDLLECCADRADLAKYICENQDSISITKLECCDKPVLEKSOCLAEVERDELPG 324
QY 301 DLPSLAADVESKDVCKNYAEAKDVFGLMFLYETARRHPDYSVLLLRLLAKTYTETLEK 360
DB 325 DLPSLAADVESKDVCKNYAEAKDVFGLMFLYETARRHPDYSVLLLRLLAKTYTETLEK 384
QY 361 CAAADPHECYAKVDFEKFPLVEEPQNLIKONCELFQOLGEYKQNALLYRYTKVQVST 420
DB 385 CATDDPTCYAKVLDLDFKPLVDEPNLVTNCELFQOLGEYKQNALLYRYTKVQVST 444
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNOLCVLHEKTPVSDRYTKCTES 480
DB 445 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNOLCVLHEKTPVSDRYTKCTES 504
QY 481 LVNRRPCFSALAEVDYTPKFEFNAETFTFHADICTLSERQIKTKOTALVELVKKPKAT 540

RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Barry T., Power S., Gannon F.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Hilger C., Grigioni F., de Beaufort C., Michel G., Hentges F.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-32.
RX MEDLINE=80024278; PubMed=488109;
RA McGilivray R.T.A., Chung D.W., Davie E.W.;
RT "Biosynthesis of bovine plasma proteins in a cell-free system. Amino-terminal sequence of prealbumin.";
RL Eur. J. Biochem. 98:477-485(1979).
RN [5]
RP SEQUENCE OF 25-424 AND 429-607.
RA Brown J.R.;
RT "Structure of bovine serum albumin.";
RL Fed. Proc. 34:591-591(1975).
RN [6]
RP REVISIONS TO 190-195.
RA Brown J.R.;
RL Submitted (APR-1975) to the PIR data bank.
RN [7]
RP SEQUENCE OF 402-433.
RX MEDLINE=82023364; PubMed=7283978;
RA Reed R.G., Putnam F.W., Peters T. Jr.;
RT "Sequence of residues 400-403 of bovine serum albumin.";
RL Biochem. J. 191:867-868(1980).
RN [8]
RP SEQUENCE OF 19-28.
RX MEDLINE=77134075; PubMed=843354;
RA Patterson J.E., Geller D.M.;
RT "Bovine microsomal albumin: amino terminal sequence of bovine prealbumin.";
RL Biochem. Biophys. Res. Commun. 74:1220-1226(1977).
RN [9]
RP SEQUENCE, AND REVISIONS TO 118-119 AND 180.
RX MEDLINE=91083649; PubMed=2260975;
RA Hirayama K., Akashi S., Furuya M., Fukuhara K.-I.;
RT "Rapid confirmation and revision of the primary structure of bovine serum albumin by ESIMS and Frit-FAB LC/MS.";
RL Biochem. Biophys. Res. Commun. 173:639-646(1990).
RN [10]
RP SEQUENCE OF 25-41.
RX MEDLINE=88267456; PubMed=3389500;
RA Hsieh J.C., Lin F.P., Tam M.F.;
RT "Electroblotting onto glass-fiber filter from an analytical isoelectrofocusing gel: a preparative method for isolating proteins for N-terminal microsequencing.";
RL Anal. Biochem. 170:1-8(1988).
RN [11]
RP SEQUENCE OF 437-451.
RA Vilbois F.;
RL Submitted (AUG-1998) to the SWISS-PROT data bank.
RN [12]
RP DISULFIDE BONDS.
RA Brown J.R.;
RT "Structure of serum albumin: disulfide bridges.";
RL Fed. Proc. 33:1389-1389(1974).
CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD BINDING CAPACITY FOR WATER, CA⁺⁺, NA⁺, K⁺, FATTY ACIDS, HORMONES, BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
CC -1- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC -----
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CC -----
DR EMBL; M73993; AAA51411.1; -;
DR EMBL; X58989; CAA41735.1; -;
DR EMBL; Y17769; CAA76847.1; -;
DR PIR; A38885; ABBOS.
DR HSP; P02768; 1E7B.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Plasma; Albumin; Metal-binding; Lipid-binding; Repeat; Signal;
KW Copper; Allergen.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 607 SERUM ALBUMIN.
FT DOMAIN 25 204 ALBUMIN 1.
FT DOMAIN 211 396 ALBUMIN 2.
FT DOMAIN 403 594 ALBUMIN 3.
FT METAL 27 27 COPPER (BY SIMILARITY).
FT DISULFID 77 86
FT DISULFID 99 115
FT DISULFID 114 125
FT DISULFID 147 192
FT DISULFID 191 200
FT DISULFID 223 269
FT DISULFID 268 276
FT DISULFID 288 302
FT DISULFID 301 312
FT DISULFID 339 384
FT DISULFID 383 392
FT DISULFID 415 461
FT DISULFID 460 471
FT DISULFID 484 500
FT DISULFID 499 510
FT DISULFID 537 582
FT DISULFID 581 590
FT CONFLICT 214 214
FT CONFLICT 302 302
FT CONFLICT 304 305
FT CONFLICT 324 324
FT CONFLICT 394 395
FT CONFLICT 437 437
FT CONFLICT 493 494
FT CONFLICT 607 AA; 69293 MW; 39167DFE768585D4 CRC64;
SQ SEQUENCE 607 AA; 69293 MW; 39167DFE768585D4 CRC64;

Query Match 79.0%; Score 2450.5; DB 1; Length 607;
Best Local Similarity 75.8%; Pred. No. 9.4e-153;
Matches 442; Conservative 71; Mismatches 69; Indels 1; Gaps 1;

QY 1 DAHKSEVAHREFKGLGEEFKALVLIATFAQYLOQCFFEDHVKLVNVEVTFEFAKTCVADESAE 60
DB 25 DTHKSEIAHREFKDLGEEHFKGLVLIATFAQYLOQCFFEDHVKLVNVEVTFEFAKTCVADES 84

QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPILPRLVPRPV 120
DB 85 GCEKSLHTLFGDELCKVASLRETYGDMADCCQPERNECFLSHKDDSPDLKPKL-KPDP 143

QY 121 DVMCTAFHNDNEETFKUKLYEIAIRHPHYFAPPELLFFAKRYKAAFTCCQAADKACLLP 180
DB 144 NTLCDFFKADEKKEKWKYLYEIAIRHPHYFAPPELLYYANKYNGVFQECQCAEDKACLLP 203

QY 181 KLDLDRDEKASSAKQRLKCSLOKGFRAFKAWAVARLSQRFKAEVSKLYDTLTK 240
DB 204 KIETNRKVLASSAKQRLKCSLOKGFRAFKAWAVARLSQRFKAEVSKLYDTLTK 263

QY 241 VHTCCCHGDLLECADRADLAKYICENODSISSKLKCECKPLLEKSHCIAEVENDMPA 300

Db 264 VHKECCGDLLECAADDRADLAKVTCNDQDTISSKLEKCCDKPLLEKSHCAEVEKDAIPE 323
QY 301 DLPSLAADFVESKDVCKNYAEADVFLGMLFYEARHPDYSVVLLRLAKTETTTLEKC 360
Db 324 NLPLTADFADKDVCKNYOQDAFGLSFLYESSRHPDYAVSVLLRLAKYEATLEEC 383
QY 361 CAADAPHECYAKVDFEKPVEEPQNLKQNCLEFQOLGKYKFNALLVRYTKVPOVST 420
Db 384 CAKDDPHACVSTVFDKHLVDEPNLKNQCDQFELGEGYFQNALVRYTKVPOVST 443
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKCCTES 480
Db 444 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSEKVTCKCTES 503
QY 481 LVNRRFCFSALEVDEYVVPKFEFNAETFFHADICTLSEKEROIKKQATLVLYVKKHPKAT 540
Db 504 LVNRRFCFSALEVDEYVVPKFEFNAETFFHADICTLSEKEROIKKQATLVLYVKKHPKAT 563
QY 541 KEOLKAVMDDFAAVFEKCKKADKDKTCFAEKGKLVAAASAAAL 583
Db 564 EEQLKTVMENFVAFVCKCAADKDEACFAVEGPKLVVSTQATL 606

RESULT 7
ALBU_RABIT STANDARD; PRT; 608 AA.
AC P49065;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxId:9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-New Zealand white; TISSUE=Liver;
RA Sheffield W.P., Syed S., Schuyler P.D.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC BINDING CAPACITY FOR WATER, CA⁺⁺, NA⁺, K⁺, FATTY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
CC -1- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC
CC EMBL; U18344; AAB58347.1; -;
CC HSSP; P02768; 1E7B.
CC InterPro; IPR000264; Serum_albumin.
CC Pfam; PF00273; transport_prot; 3.
CC PRINTS; PR00802; SERUMALBUMIN.
CC ProDom; PD002486; Serum_albumin; 1.
CC SMART; SM00103; ALBUMIN; 3.
CC PROSITE; PS00212; ALBUMIN; 3.
CC Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW Copper.
KW SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 24 BY SIMILARITY.
FT CHAIN 25 608 SERUM ALBUMIN.
FT DOMAIN 25 205 ALBUMIN 1.

FT DOMAIN 212 397 ALBUMIN 2.
FT DOMAIN 404 595 ALBUMIN 3.
FT METAL 27 27 COPPER.
FT DISULFID 77 96 BY SIMILARITY.
FT DISULFID 99 115 BY SIMILARITY.
FT DISULFID 114 125 BY SIMILARITY.
FT DISULFID 148 193 BY SIMILARITY.
FT DISULFID 192 201 BY SIMILARITY.
FT DISULFID 224 270 BY SIMILARITY.
FT DISULFID 269 277 BY SIMILARITY.
FT DISULFID 289 303 BY SIMILARITY.
FT DISULFID 302 313 BY SIMILARITY.
FT DISULFID 340 385 BY SIMILARITY.
FT DISULFID 384 393 BY SIMILARITY.
FT DISULFID 416 462 BY SIMILARITY.
FT DISULFID 461 472 BY SIMILARITY.
FT DISULFID 485 501 BY SIMILARITY.
FT DISULFID 500 511 BY SIMILARITY.
FT DISULFID 538 583 BY SIMILARITY.
FT DISULFID 582 591 BY SIMILARITY.
SQ SEQUENCE 608 AA; 68914 MW; CF5E92647AAFE9A2 CRC64;
Query Match 78.8%; Score 2446; DB 1; Length 608;
Best Local Similarity 74.1%; Pred. No. 1.9e-152;
Matches 433; Conservative 77; Mismatches 74; Indels 0; Gaps 0;
QY 1 DAHSEVAREFKDGLGENFKALVIAFAOYLQCCPPEDHVKLVNEVTEFAKTCVADESAAE 60
Db 25 EAHKSEIAHFRNDVGEHFGLVITFSQYLQKCPVEEHAKLVKEVTDLAKACVADESAA 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPEERNECFLOHKDDNPNLRLVRPE 120
Db 85 NCDKSLHDFDGLKICALPSLRTDYGVDACCCKEPEERNECFLOHKDDNPNLRLVRPEA 144
QY 121 DVMCTAFHNEETFLAKLYLEIARRHPYFYAPPELLFPKRYKAAFTTCCQAADKAACLLP 180
Db 145 DVLCKAFPHDDEKAFHGHLYEVARHPYFYAPPELLYAAQRYKAILTECCBAADKAGACLTP 204
QY 181 KLDELDEGKASSAKORLKCASLQKGERAFKAWARLVARLQSFPAEFAVSVLVTDLTK 240
Db 205 KLDALSGKSLISAAQERLRCASIQKFGDRAYKAWALVLSORFPKADFTDISKIVTDLTK 264
QY 241 VHTECCGDLLECAADDRADLAKVTCNDQDTISSKLEKCCDKPLLEKSHCAEVEKDAIPE 300
Db 265 VHKECCGDLLECAADDRADLAKVTCNDQDTISSKLEKCCDKPLLEKSHCAEVEKDAIPE 324
QY 301 DLPSLAADFVESKDVCKNYAEADVFLGMLFYEARHPDYSVVLLRLAKTETTTLEKC 360
Db 325 GLPAVAEEFVEDKDVCKNYEAEKDLFLGKFLYESSRHPDYAVSVLLRLAKYEATLEEC 384
QY 361 CAADAPHECYAKVDFEKPVEEPQNLKQNCLEFQOLGKYKFNALLVRYTKVPOVST 420
Db 385 CATDDPHACVSTVFDKHLVDEPNLKNQCDQFELGEGYFQNALVRYTKVPOVST 444
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKCCTES 480
Db 445 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSEKVTCKCTES 504
QY 481 LVNRRFCFSALEVDEYVVPKFEFNAETFFHADICTLSEKEROIKKQATLVLYVKKHPKAT 540
Db 505 LVNRRFCFSALEVDEYVVPKFEFNAETFFHADICTLSEKEROIKKQATLVLYVKKHPKAT 564
QY 541 KEOLKAVMDDFAAVFEKCKKADKDKTCFAEKGKLVAAASAAALG 584
Db 565 NDQLKTVVGEFTALLDKCCSAEDKEACFAVEGPKLVVSTQATLG 608
RESULT 8
ALBU_SHEEP STANDARD; PRT; 607 AA.
ID ALBU_SHEEP
AC P14639;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)
Serum albumin precursor.

ALB.
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Hovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
[1]
SEQUENCE FROM N.A.
TISSUE=Liver;
MEDLINE=9009888; PubMed=2602160;
Brown W.M., Dziegielewska K.M., Foreman R.C., Saunders N.R.;
"Nucleotide and deduced amino acid sequence of sheep serum albumin."
Nucleic Acids Res. 17:10495-10495(1989).
-!- FUNCTION: SERUM ALBUMIN. THE MAIN PROTEIN OF PLASMA, HAS A GOOD
BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: PLASMA.
-!- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
-!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.

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or send an email to license@isb-sib.ch).

EMBL; X17055; CAA34903.1; .
PIR; S06936; ABSHS.
HSP; P02768; 1E7B.
InterPro; IPR000264; Serum_albumin.
Pfam; PF00273; transport_prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
PRODOM; P002486; Serum_albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
Copper.

FT SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 24 BY SIMILARITY.
FT CHAIN 25 207 SERUM ALBUMIN.
FT DOMAIN 25 204 ALBUMIN 1.
FT DOMAIN 211 396 ALBUMIN 2.
FT DOMAIN 403 594 ALBUMIN 3.
FT METAL 27 27 COPPER (BY SIMILARITY).
FT METAL 77 86 COPPER (BY SIMILARITY).
FT DISULFID 99 115 BY SIMILARITY.
FT DISULFID 114 125 BY SIMILARITY.
FT DISULFID 147 192 BY SIMILARITY.
FT DISULFID 191 200 BY SIMILARITY.
FT DISULFID 223 269 BY SIMILARITY.
FT DISULFID 268 276 BY SIMILARITY.
FT DISULFID 288 302 BY SIMILARITY.
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FT DISULFID 339 384 BY SIMILARITY.
FT DISULFID 383 392 BY SIMILARITY.
FT DISULFID 415 461 BY SIMILARITY.
FT DISULFID 460 471 BY SIMILARITY.
FT DISULFID 484 500 BY SIMILARITY.
FT DISULFID 499 510 BY SIMILARITY.
FT DISULFID 537 582 BY SIMILARITY.
FT DISULFID 581 590 BY SIMILARITY.
FT SEQUENCE 607 AA; 69188 MW; 84979A87F8B86596 CRC64;

Query Match 78.4%; Score 2432.5; DB 1; Length 607;
Best Local Similarity 75.0%; Pred. No. 1.4e-151;
Matches 437; Conservative 73; Mismatches 72; Indels 1; Gaps 1;

QY 1 DAHKSEVAHRKDLGEENFKALVLIATFAOYLQCCPFEDHVKLVNVEYTERAKTCVADESAB 60
DB 25 DTHKSEIAHRFNDLGEENFQGLVLIATFAOYLQCCPFEDHVKLVNVEYTERAKTCVADESAB 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECELOHKKDDNPRLVRPEV 120
DB 85 GCDKSLHTLFGDELCKVATLRETYGDMADCCKEQEPERNECEFNHKKDDSPDLPKL-KPEP 143
QY 121 DVMTAFADHNEETFLKYLKYEIARRHPYFAPLELFFAKRYKAAFTTECCQAADKACCLLP 180
DB 144 DTLCAEFKADKKFWGKYLKYEIARRHPYFAPLELFIYANKYNGVFQCCQADKACCLLP 203
QY 181 KIDELRDGKASSAKORLKASLQKGERAFKAWARLARSQRPKAEFAEYSLKLYDTLTK 240
DB 204 KIDAMREKVLASSARQLRCASIQKGERALKAWSARLSQKFPKADFDTVTIKVITDLTK 263
QY 241 VHTCECHGDLLECADDRADLAKYICENODSISSKKECEKPLLEKSHCIAEVENDEMPA 300
DB 264 VHKCECHGDLLECADDRADLAKYICDHQDALSSKKECCDKPVLEKSHCIAEVDKDAVPE 323
QY 301 DLPSLAADFVESKDYCKNVAEAKDVLGMFLYKYEIARRHPDYVWLLLRLLAKTYETTLK 360
DB 324 NLPPLTADFADKVECKNVAEAKDVLGMFLYKYEIARRHPDYVWLLLRLLAKTYETTLK 383
QY 361 CAADPHCYAKVDFEFLVPEEPQNLKQNCLEFQELGEYKFNALLVRYTKVPQVST 420
DB 384 CAKEDPHACYATVDFKHLVDPEQNLKQNCLEFQELGEYKFNALLVRYTKVPQVST 443
QY 421 PTLVEVRNLGKVGSKCKHPKAPKAEADYLSVVLNOLCVLHEKTPVSDRYTKCCTES 480
DB 444 PTLVVISRSLGKVGKCKKAPKAEADYLSVVLNOLCVLHEKTPVSEKTVKCTES 503
QY 481 LVNRRPCFSALEVDFTYVPKPENAETFFHADICTLSEKEROIKKOTALVELVVKHKPRAT 540
DB 504 LVNRRPCFSDLTDETYVPKPEDEKFFTHADICTLSEKEROIKKOTALVELVVKHKPRAT 563
QY 541 KEOLKAVMDFAAFVEKCKKADKTCFAEGKGLVAASQAAL 583
DB 564 DEQLKVTMENFVAFVDKCCAADKKEGCFVLEGPKLVAASQAAL 606
RESULT 9
ID ALBU_RAT STANDARD; PRT: 608 AA.
AC P02770; P11382;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor [Contains: Neurotensin-related peptide (NRP)].
GN ALB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8123722; PubMed=7017712;
RA Sargent T.D., Yang M., Bonner J.;
RT "Nucleotide sequence of cloned rat serum albumin messenger RNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:243-246(1981).
RN [2]
RP SEQUENCE OF 1-38, AND PROCESSING.
RX MEDLINE=77249657; PubMed=893447;
RA Strauss A.W., Bennett C.D., Donohue A.M., Rodkey J.A., Alberts A.W.;
RT "Rat liver pre-proalbumin: complete amino acid sequence of the pre-
piece. Analysis of the direct translation product of albumin
messenger RNA.";
RL J. Biol. Chem. 252:6846-6855(1977).
RN [3]
RP SEQUENCE OF 25-222.
RX MEDLINE=78109429; PubMed=564345;
RA Isemura S., Ikenaka T.;
RT "Amino acid sequences of fragments I and II obtained by cyanogen

bromide cleavage of rat serum albumin.";
[4]
SEQUENCE OF 223-288 AND 572-608.
MEDLINE=76260153; PubMed=956149;
Isemura S., Ikenaka T.;
"Fragmentation of rat serum albumin by cyanogen bromide cleavage and
the amino acid sequences of four fragments.";
J. Biochem. 79:1183-1196(1976).
[5]
SEQUENCE OF 166-174.
TISSUE=Plasma;
MEDLINE=87194805; PubMed=2437111;
Carraway R.E., Mitra S.P., Cochrane D.E.;
"Structure of a biologically active neurotensin-related peptide
obtained from pepsin-treated albumin(s).";
J. Biol. Chem. 262:5968-5973(1987).
[6]
COPPER-BINDING.
MEDLINE=79001617; PubMed=80265;
Aoyagi Y., Ikenaka T., Ichida F.;
"Copper(II)-binding ability of human alpha-fetoprotein.";
Cancer Res. 38:3483-3486(1978).
CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -1- FUNCTION: NRP REGULATES FAT DIGESTION, LIPID ABSORPTION, AND
BLOOD FLOW (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -1- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.

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or send an email to license@isb-sib.ch).

DR EMBL; V01222; CAA24532.1; -;
DR PIR; A03233; ABRTS.
DR HSP; P02768; IE7B.
DR InterPro: IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR PRODOM; PD002486; Serum_albumin.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW Copper.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 608 SERUM ALBUMIN.
FT PEPTIDE 166 174 NEUTROTENSIN-RELATED PEPTIDE.
FT DOMAIN 25 205 ALBUMIN 1.
FT DOMAIN 212 397 ALBUMIN 2.
FT DOMAIN 404 595 ALBUMIN 3.
FT METAL 27 27 COPPER.
FT DISULFID 77 86 BY SIMILARITY.
FT DISULFID 99 115 BY SIMILARITY.
FT DISULFID 114 125 BY SIMILARITY.
FT DISULFID 148 193 BY SIMILARITY.
FT DISULFID 192 201 BY SIMILARITY.
FT DISULFID 224 270 BY SIMILARITY.
FT DISULFID 269 277 BY SIMILARITY.
FT DISULFID 289 303 BY SIMILARITY.
FT DISULFID 302 313 BY SIMILARITY.
FT DISULFID 340 385 BY SIMILARITY.
FT DISULFID 384 393 BY SIMILARITY.
FT DISULFID 416 462 BY SIMILARITY.

FT DISULFID 461 472 BY SIMILARITY.
FT DISULFID 485 501 BY SIMILARITY.
FT DISULFID 500 511 BY SIMILARITY.
FT DISULFID 538 583 BY SIMILARITY.
FT DISULFID 582 591 BY SIMILARITY.
FT VARIANT 262 262 V -> L.
FT CONFLICT 174 174 Y -> L (IN REF. 5).
SQ SEQUENCE 608 AA; 68718 MW; 5BB497A282411AB7 CRC64;

Query Match 78.2%; Score 2426; DB 1; Length 608;
Best Local Similarity 73.4%; Pred. No. 3.7e-151;
Matches 428; Conservative 82; Mismatches 73; Indels 0; Gaps 0;

QY 1 DAHKSEVAHFKDGLGEENFKALVLIAPAFQVLQCCPFEDHVKLVNEVTEFAKTCVADSAE 60
DB 25 EAHKSEIAHFKDGLGEQHFGLVLIASFQYLQKCPYEHKLVQEVTFDAKTCVADENAE 84

QY 61 NCDKSLHTLFEGDGLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPLVRPEV 120
DB 85 NCDKSIHTLFEGDKLCAIPKLRDNYGELADCCAKQEPERNECFLOHKDDNPNLPPQRPEA 144

QY 121 DVMTAFHNEETFLKKLYEIAARRHPFYFAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
DB 145 EAMCTSFQENPTFLGHYLHEVARHPFYFAPPELLLYAERYNEVLTQCCSTESDKAACLT 204

QY 181 KLDELREGKASSAKORLKCASLQKFGERAFKAWARLRSORFPKAEFAEVSKLVTLDTLK 240
DB 205 KLDVKEKALVAVRQRMKCSSMORFGERAFKAWARMSORFPNAEFAITKLATDVTK 264

QY 241 VHTCCGDLLECCADRADLAKYICENQDSISLKECKECPLEKSHCIAEVENDEMPA 300
DB 265 INKECCHGDLLECCADRAELAKYMCENQATISSKLOACCDKPVLOKSOCLAETEDHNIPA 324

QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMPLEYEARHPDYSVVLRLAKTYETITLEK 360
DB 325 DLPSIAADFVEDKVCNKYAEAKDVLGTLFELYSRRHPDYSVSLRLAKKYEATLEK 384

QY 361 CAAADHECVAKYVDFEKLVEPQNLIKONCELFQGLGEYKFNQALLVRYTKVPOVST 420
DB 385 CAGSDPPACVGTVLAEPQLVEEPKLVKTNCELYEKLGEYQNAVLYRYTKAPOVST 444

QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 445 PTLVEAARNLGRVGTCKCTLPEAORLPCVEDYLSAILNRLCVLHEKTPVSEKVTCKCSGS 504

QY 481 LVNRRPCFSALEVDETYVPKEFNAETFFHADICTLSEKERQIKQTALVELYKHKPKAT 540
DB 505 LVERRPCFSALTVDETYVPKEFNAETFFHSDICTLPDKEKQIKQTALAEVLKHKPKAT 564

QY 541 KEOLKAVMDDFAAVFEKCKCKADDKETCFAEEGKLVAAASOAL 583
DB 565 EDQLKTVMGDFQFVDKCKCKADKDNCFATEGNLVARSKAL 607

RESULT 10
ALBU_PIG STANDARD; PRT; 605 AA.
ID ALBU_PIG Q29018;
AC P08835; Q29018;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor (Fragment).
GN ALB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89016582; PubMed=3174440;
RA Baldwin G.S., Weinstein J.;
RT "Nucleotide sequence of porcine liver albumin.";

DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SMO0103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW Copper.

```
FT SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 24 BY SIMILARITY.
FT CHAIN 25 609 SERUM ALBUMIN.
FT FT 25 609 CHAIN
FT DOMAIN 25 206 ALBUMIN 1.
FT FT 213 398 ALBUMIN 2.
FT DOMAIN 405 596 ALBUMIN 3.
FT FT 28 28 COPPER.
FT METAL 78 87 BY SIMILARITY.
FT DISULFID 100 116 BY SIMILARITY.
FT DISULFID 115 126 BY SIMILARITY.
FT DISULFID 149 194 BY SIMILARITY.
FT DISULFID 193 202 BY SIMILARITY.
FT DISULFID 225 271 BY SIMILARITY.
FT DISULFID 270 278 BY SIMILARITY.
FT DISULFID 290 304 BY SIMILARITY.
FT DISULFID 303 314 BY SIMILARITY.
FT DISULFID 341 386 BY SIMILARITY.
FT DISULFID 385 394 BY SIMILARITY.
FT DISULFID 417 463 BY SIMILARITY.
FT DISULFID 462 473 BY SIMILARITY.
FT DISULFID 486 502 BY SIMILARITY.
FT DISULFID 501 512 BY SIMILARITY.
FT DISULFID 539 584 BY SIMILARITY.
FT DISULFID 583 592 BY SIMILARITY.
SQ SEQUENCE 609 AA; 68940 MW; 9CA5F97F67EF1A48 CRC64;

Query Match 76.9%; Score 2387; DB 1; Length 609;
Best Local Similarity 73.9%; Pred. No. 1.3e-148;
Matches 430; Conservative 65; Mismatches 87; Indels 0; Gaps 0;

QY 2 AHKSEVAHFKDGEENFKALVIAFYAQYLOQCFPDHVKLVNEVTEFAKTCVADESAEN 61
Db 27 AHKSEIAHRYKDLGKEYFKGLVLYTFQYLOKCSYEBHVKLVREVTDFASNAKDESAEN 86
QY 62 CDKSLHPTLFGDKLCTVATLRETGEMADCCAKQEPERNECFLOHKDNDPNLRLVREPD 121
Db 87 CDKSLHPTLFGDKLCTVATLRETGEMADCCAKQEPERNECFLOHKDNDPNLRLVREPD 146
QY 122 VMCTAFHDNEETFLKLYLTIARRHPYFYAPPELLFFAKRYKAAAFTECCQAADKAACLLPK 181
Db 147 AMCTAFQENAEAFMGHLYHEVARHPYFYCGPELLYADKYTAVLTECCADDDKGCACITPK 206
QY 182 LDELRDGKASSAKQRLKASLOKFGRAKNAVARLSORFPAEYKSVKLVTDLTKV 241
Db 207 LDALKERKALYSVRQRLKCSMKKFGRAKNAVARMSOTFPNADPAETTKLATDLTKV 266
QY 242 HTECCHGDLLECCADDRADLAKYICENODSTSSKLKCECKPLLEKSHCIAEVENDEMPAD 301
Db 267 TQECCHGDLLECCADDRADLAKYICENODSTSSKLKCECKPLLEKSHCIAEVENDEMPAD 326
QY 302 LPSLAADFESKDYCKNYABAKDFVGLMFLYEXARRHPDYSVVLLRLAKLYETTTLEKCC 361
Db 327 LPALTADVEDKDKCKNYABAKDFVGLMFLYEXARRHPDYSVVLLRLAKLYETTTLEKCC 386
QY 362 AADPHCEYAKVDFDEFPVLEEONLIKQNCLEFEQLGEYKFNALLVRYTKVPQVSTP 421
Db 387 AADPHCEYAKVDFDEFPVLEEONLIKQNCLEFEQLGEYKFNALLVRYTKVPQVSTP 446
QY 422 TLVEVSRLNKGSKCKHPEAKRMPCAEADYLSVVLNQLCVLHEKTPVSDRVTKCCETSL 481
Db 447 TLVEAARSLGRVTHCCALPEKRLPCVEDYLSAILNRVCLLHEKTPVSDRVTKCCGSL 506
QY 482 VNRPCFSALEVDYVYPKEAFETTFHADICTLSEKERQIKQATLALVELVKKPKATK 541
Db 507 VERRPCFSALEVDYVYPKEAFETTFHADICTLSEKERQIKQATLALVELVKKPKATK 566
QY 542 EQLKAYMDDFAAFVEKCCAKDDKTCFAEFGKLVVAASQAAL 583
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Db 567 EQLKVMGDFAEFLKCKCKQEDKEACFSTEGPKLVAESQKAL 608

RESULT 12

ALBU_MOUSE

ID ALBU_MOUSE STANDARD; PRT; 608 AA.

AC P07724; Q61802;

DT 01-APR-1988 (Rel. 07, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Serum albumin precursor.

GN ALB OR ALBI.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA van Reeth T., Gabant P., Dreze P., Szpirer J., Szpirer C.;

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Tongue;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Harai A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojohori T., Hono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

RP SEQUENCE OF 99-516 FROM N.A.

RX MEDLINE=88216123; PubMed=2452956;

RA Minghetti P.P., Law S.W., Dugaiczky A.;

RT "The rate of molecular evolution of alpha-fetoprotein approaches that

RT of pseudogenes.";

RL Mol. Biol. Evol. 2:347-358(1985).

RN [4]

RP SEQUENCE OF 477-551 FROM N.A.

RC STRAIN=BALB/C;

RX MEDLINE=90269606; PubMed=1971802;

RA Bocaccio C., Deschattrette J., Meunier-Rotival M.;

RT "Empty and occupied insertion site of the truncated LINE-1 repeat

RT located in the mouse serum albumin-encoding gene.";

RL Gene 88:181-186(1990).

RN [5]

RP SEQUENCE OF 25-44.

RC TISSUE=Liver;

RX MEDLINE=93162044; PubMed=1286668;

RA Giometti C.S., Taylor J., Tollaksen S.L.;

RT "Mouse liver protein database: a catalog of proteins detected by two-

RT dimensional gel electrophoresis.";

RL Electrophoresis 13:970-991(1992).

CC -I- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD

CC BINDING CAPACITY FOR WATER, CA⁺⁺, NA⁺, K⁺, FATTY ACIDS, HORMONES,

CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE

CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.

CC -I- SUBCELLULAR LOCATION: Secreted.

FT	DOMAIN	212	397	ALBUMIN 2.
FT	DOMAIN	404	595	ALBUMIN 3.
FT	METAL	22	22	COPPER AND NICKEL (BY SIMILARITY).
FT	DISULFID	99	114	BY SIMILARITY.
FT	DISULFID	113	124	BY SIMILARITY.
FT	DISULFID	148	193	BY SIMILARITY.
FT	DISULFID	192	201	BY SIMILARITY.
FT	DISULFID	224	270	BY SIMILARITY.
FT	DISULFID	269	277	BY SIMILARITY.
FT	DISULFID	289	303	BY SIMILARITY.
FT	DISULFID	302	313	BY SIMILARITY.
FT	DISULFID	384	393	BY SIMILARITY.
FT	DISULFID	416	462	BY SIMILARITY.
FT	DISULFID	461	472	BY SIMILARITY.
FT	DISULFID	485	501	BY SIMILARITY.
FT	DISULFID	500	511	BY SIMILARITY.
FT	DISULFID	538	583	BY SIMILARITY.
FT	DISULFID	582	591	BY SIMILARITY.
FT	CARBOHYD	42	42	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	251	251	N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE	609 AA; 68741 MW; C032987CAD0E672B CRC64;		

Query Match

40.4%; Score 1253.5; DB 1; Length 609;

Best Local Similarity 40.1%; Pred. No. 1.1e-74;

Matches 236; Conservative 115; Mismatches 231; Indels 7; Gaps 3;

QY	3	HKSE-----VAHFKDILGEENFKALVLI	FAQVLOQCPFEDHVKLVN	TEFAKTCVADE	57							
Db	22	HRNEYGIASILD	SYCTAEINLTDLATIFFAQVQVQATYKEVYSK	MVKDALTAEKPTGDE	81							
QY	58	SAENCKSLHTL	FGDKLCVATLRETYGEMADCCAKQEPERNEC	FLQHKDDNP-NLPR	116							
Db	82	QSAGCLENQ	LPALBELCREKELEKYGH-SDCCS	SEGRHNCFLA	HKKPTPASIPFQ	140						
QY	117	RPEVDMCAF	HDNETFLKYL	YETARRHPYF	YAPELIFFAKRY	KAATECCQAAADKAA	176					
Db	141	VPEPVTSC	EAYEDRETFM	KFTYEIARRHP	FLYAKTILLIWA	RYDKIIPSCCKAENAVE	200					
QY	177	CLLPKLDEL	RDCKASSAKOR	LKASLOKGERAF	AKAWARLSOR	FPKPAEVSCLYT	236					
Db	201	CFOTKAA	TVTKLEURESS	LLNQHACAV	MKNFGTRTFO	AITVTKLSQKFTK	VNFTEIOKLVL	260				
QY	237	DLTKVHT	ECGDLLECAD	DRADLAKYIC	ENQDSISSKL	KECEKPLLEKSH	CHIAEVEND	296				
Db	261	DVAHVH	ECRGVLDCL	QGEKIMYS	CSQDITLSN	KITECCKLTL	ERGQCIHAEND	320				
QY	297	EMPADL	PSLAADP	VEKDKVNA	EAKDVLGM	FLYEARHP	PDYSVLLRLAKTYET	356				
Db	321	EKPEGL	SNLNRFL	GBDRF	NQFSG	SEKFNIFLAS	FVHEYSRRHP	QLAVSVILRVAKGYQEL	380			
QY	357	LEKCCAA	ADPHECYA	KVDFE	KPLVEP	ONLIKONCE	LPOLGEYKFON	ALLVRYTKVP	416			
Db	381	LEKCFOT	ENPLECQD	GEELQYI	QESALARS	CGLFQK	GEYQLQNA	FLVAYTKAP	440			
QY	417	QVSTPTL	VEYSNRLG	VGSKCR	KHPKAE	RMPCAE	DYLSVVLN	OLCVLHETKTPV	SDRVTK	476		
Db	441	QLTSS	ELMALTR	KWATA	TCCQLSE	DKLLAC	EGEAGADI	IIGHLCIR	HETTPVNP	CGVQC	500	
QY	477	CTSLVNR	PCFSALE	VDYVP	KENAE	TFTPH	ADICLSE	KEROIK	KTOTAL	VELVKH	536	
Db	501	CTSSYAN	RRPCF	SSLVVD	YTPV	PAFSD	DKFIF	HKDLC	QAQGV	ALQTMKQ	FLINLVKQ	560
QY	537	PKATK	EOALVMD	DAFA	VEKCK	ADKDK	ETCF	AEKGL	KLVA	ASQA	ALGL	585
Db	561	POITE	EOLEAV	IA	ADFSG	LLKCCQ	GGQEQE	VCFAE	BGOKL	ISKTR	AALGV	609

RESULT 15

FETA_HUMAN

ID FETA_HUMAN

STANDARD; PRT; 609 AA.

AC P02771;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT	15-JUN-2002	(Rel. 41, Last annotation update)
DE	Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-fetoprotein).	
DE	AFP.	
GN	Homo sapiens (Human).	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OC	NCBI_TaxID=9606;	
OX	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=83273664; PubMed=6192439;	
RA	Morinaga T., Sakai M., Wegmann T.G., Tamaoki T.;	
RT	"Primary structures of human alpha-fetoprotein and its mRNA.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 80:4604-4608(1983).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=87185438; PubMed=2436661;	
RA	Gibbs P.E.M., Zielinski R., Boyd C., Dugaiczak A.;	
RT	"Structure, polymorphism, and novel repeated DNA elements revealed by a complete sequence of the human alpha-fetoprotein gene.";	
RL	Biochemistry 26:1332-1343(1987).	
RN	[3]	
RP	SEQUENCE OF 1-28 FROM N.A.	
RX	MEDLINE=93278385; PubMed=7684942;	
RA	Mcvey J.H., Michaelides K., Hansen L.P., Ferguson-Smith M., Tilghman S., Krumlauf R., Tuddenham E.G.D.;	
RT	"A G->A substitution in an HNF I binding site in the human alpha-fetoprotein gene is associated with hereditary persistence of alpha-fetoprotein (HPAFP).";	
RL	Hum. Mol. Genet. 2:379-379(1993).	
RN	[4]	
RP	SEQUENCE OF 429-556 FROM N.A.	
RX	MEDLINE=83158778; PubMed=6187626;	
RA	Beattie W.G., Dugaiczak A.;	
RT	"Structure and evolution of human alpha-fetoprotein deduced from partial sequence of cloned cDNA.";	
RL	Gene 20:415-422(1982).	
RN	[5]	
RP	PARTIAL SEQUENCE OF 19-609.	
RX	MEDLINE=91242409; PubMed=1709810;	
RA	Pucci P., Siciliano R., Malorni A., Marino G., Tecce M.F., Ceccarini C., Terrana B.;	
RT	"Human alpha-fetoprotein primary structure: a mass spectrometric study.";	
RL	Biochemistry 30:5061-5066(1991).	
RN	[6]	
RP	PRELIMINARY SEQUENCE OF 19-35.	
RX	MEDLINE=77242506; PubMed=70228;	
RA	Yachnin S., Hsu R., Heinrichson R.L., Miller J.B.;	
RT	"Studies on human alpha-fetoprotein. Isolation and characterization of monomeric and polymeric forms and amino-terminal sequence analysis.";	
RL	Biochim. Biophys. Acta 493:418-428(1977).	
RN	[7]	
RP	PRELIMINARY SEQUENCE OF 19-38.	
RX	MEDLINE=78001760; PubMed=711198;	
RA	Aoyagi Y., Ikenaka T., Ichida F.;	
RT	"Comparative chemical structures of human alpha-fetoproteins from fetal serum and from ascites fluid of a patient with hepatoma.";	
RL	Cancer Res. 37:3663-3667(1977).	
RN	[8]	
RP	PRELIMINARY SEQUENCE OF 19-39.	
RX	MEDLINE=75018719; PubMed=4138095;	
RA	Ruostelahti E., Pihko H., Vaheri A., Seppala M., Virolainen M., Kontinen A.;	
RT	"Alpha fetoprotein: structure and expression in man and inbred mouse strains under normal conditions and liver injury.";	
RL	Johns Hopkins Med. J. Suppl. 3:249-255(1974).	
RN	[9]	
RP	GENE STRUCTURE.	
RX	MEDLINE=85182629; PubMed=2580830;	
RA	Sakai M., Morinaga T., Urano Y., Watanabe K., Wegmann T.G., Tamaoki T.;	

"The human alpha-fetoprotein gene. Sequence organization and the 5' flanking region.";
 J. Biol. Chem. 260:5055-5060(1985).
 [10]
 RN METAL-BINDING.
 RX MEDLINE-79001617; PubMed-80265;
 RA Aoyagi Y., Ikenaka T., Ichida F.;
 RT "Copper(II)-binding ability of human alpha-fetoprotein.";
 RL Cancer Res. 38:3483-3486(1978).
 [11]
 RN BILIRUBIN-BINDING.
 RX MEDLINE-80001710; PubMed-89900;
 RA Aoyagi Y., Ikenaka T., Ichida F.;
 RT "Alpha-Fetoprotein as a carrier protein in plasma and its bilirubin-binding ability.";
 RL Cancer Res. 39:3571-3574(1979).
 [12]
 RN SULFATION.
 RX MEDLINE-86042625; PubMed-2414772;
 RA Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.;
 RT "Tyrosine sulfation of proteins from the human hepatoma cell line HepG2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).
 CC -1- FUNCTION: BINDS COPPER, NICKEL, AND FATTY ACIDS AS WELL AS, AND BILIRUBIN LESS WELL THAN, SERUM ALBUMIN. ONLY A SMALL PERCENTAGE (LESS THAN 2%) OF THE HUMAN AFP SHOWS ESTROGEN-BINDING PROPERTIES.
 CC -1- SUBUNIT: DIMERIC AND TRIMERIC FORMS HAVE BEEN FOUND IN ADDITION TO THE MONOMERIC FORM.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PLASMA. SYNTHESIZED BY THE FETAL LIVER AND YOLK SAC.
 CC -1- DEVELOPMENTAL STAGE: OCCURS IN THE PLASMA OF FETUSES MORE THAN 4 WEEKS OLD, REACHES THE HIGHEST LEVELS DURING THE 12TH-16TH WEEK OF GESTATION, AND DROPS TO TRACE AMOUNTS AFTER BIRTH. THE SERUM LEVEL IN ADULTS IS USUALLY LESS THAN 40 NG/ML. AFP OCCURS ALSO AT HIGH LEVELS IN THE PLASMA AND ASCITIC FLUID OF ADULTS WITH HEPATOMA.
 CC -1- PTM: INDEPENDENT STUDIES SUGGEST HETEROGENEITY OF THE AMINO-TERMINAL SEQUENCE OF THE MATURE PROTEIN AND OF THE CLEAVAGE SITE OF THE SIGNAL SEQUENCE.
 CC -1- PTM: SULFATED.
 CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
 CC -----
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 CC -----
 DR EMBL; M10949; AAA51674.1; -;
 DR EMBL; M10950; AAA51675.1; -;
 DR EMBL; V01514; CAA24758.1; -;
 DR EMBL; M16110; AAB58754.1; -;
 DR EMBL; Z19532; CAA79592.1; -;
 DR PIR; A03234; FPHU.
 DR PIR; A26624; A26624.
 DR HSP; P02768; IE7B.
 DR GlycoSuiteDB; P02771; -;
 DR Sienra-2DPAGE; P02771; -;
 DR Genew; HGNC:317; AFP.
 DR MN; 104150; -;
 DR InterPro; IPR000264; Serum_albumin.
 DR Pfam; PF00273; transport_prot; 3.
 DR PRINTS; PR00802; SERUMALBUMIN.
 DR ProDom; PD002486; Serum_albumin; 1.
 DR SMART; SM00103; ALBUMIN; 3.
 DR PROSITE; PS00212; ALBUMIN; 2.
 DR GlycoProtein; Sulfation; Albumin; Plasma; Repeat; Metal-binding;
 KW Copper; Nickel; Signal; Polymorphism;
 FT SIGNAL 1 18
 FT CHAIN 19 609 ALPHA-FETOPROTEIN.

DOMAIN	20	205	ALBUMIN 1.
FT DOMAIN	212	397	ALBUMIN 2.
FT DOMAIN	404	595	ALBUMIN 3.
FT METAL	22	22	COPPER AND NICKEL.
FT DISULFID	99	114	
FT DISULFID	113	124	
FT DISULFID	148	193	
FT DISULFID	192	201	
FT DISULFID	224	270	
FT DISULFID	269	277	
FT DISULFID	289	303	
FT DISULFID	302	313	
FT DISULFID	384	393	
FT DISULFID	416	462	
FT DISULFID	461	472	
FT DISULFID	485	501	
FT DISULFID	500	511	
FT DISULFID	538	583	
FT DISULFID	582	591	
FT CARBOHYD	251	251	
FT VARIANT	570	570	
FT SEQUENCE	609 AA;	68677 MW;	4D4E45820E1C2D4F CRC64;
Query Match	40.3%;	Score 1249.5;	DB 1; Length 609;
Best Local Similarity	39.9%;	Pred. No. 1.9e-74;	
Matches 235;	Conservative 116;	Mismatches 231;	Indels 7; Gaps 3;

N-LINKED (GLCNAC. . .).
 /FTid-CAR_000070.
 A->G (IN DBSNP:1057173).
 /FTid-VAR_012049.
 40.3%; Score 1249.5; DB 1; Length 609;
 Best Local Similarity 39.9%; Pred. No. 1.9e-74;
 Matches 235; Conservative 116; Mismatches 231; Indels 7; Gaps 3;

QY 3 HKSE-----VAHRPKDLGEENFKALVIAFAQYLOQQPFEDHVKLVNEVTEFAKTCVADE 57
 DB 22 HRNEYGIASILDVSQTAETISLADLATITFAQFQEAITYKEVSMVKMDALTAIEKPTGDE 81
 QY 58 SAENCDLSLHTLFGDKLCTVATLRETGEMADCCAKOPEKNECFLOHKDDNP-NLRLV 116
 DB 82 QSSCLENQLPALEELCHEKEILEKYGH-SDDCSQSEGRHNCFLAHKKTPASIPULFQ 140
 QY 117 RPEYDVMACTAFHDNEETFLKKYLYEIAARRHPYFYAPELFFAKRYKAAFTCCQAADKAA 176
 DB 141 VPEPVTSCAEYEDRETFMNKFIVEIARRHPYFAPTILLWAARYDKTIIPSCCKAENAVE 200
 QY 177 CLLPKLDLREDEGKASSAKQBLKCAKQKGFERAFKAWARLRSQRPKAFKAEVSKLVT 236
 DB 201 CFQTKAATVTKELRESSLLNQHACAVMKNFGTFTFQAITVTKLSQKFTKVNFTIQKLV 260
 QY 237 DLTQVTECHGDLLECADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVEND 296
 DB 261 DVAIVHEHCRRGVLDCLQDGEKIMSYICSQODTSLNKITECCCKLTTLERQCQCIHAEND 320
 QY 297 EMPADPLSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVVLLRLAKTYETT 356
 DB 321 EKPEGLSPNLNRLGDRDFNQFSSGKNIPLASFPVHEYSRRHPQLAVSVILRVAKGYQEL 380
 QY 357 LEKCAAADPHECYAKVDFDEKPLVEEPQNLKONCELFQOLGEYKFQNALLLVRYTKVP 416
 DB 381 LEKCFOTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLGYYLQNALVAYTRKAP 440
 QY 417 QVSTPTLVEYSRNLGKVGSKCKHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRYTKC 476
 DB 441 QLTSSLMATRKMAATAATCCQLSEDKLLACGEGADIIIGHLCIRHMTVPVPGVQC 500
 QY 477 CTESLVNRRPFCFSALEVDYVVPKFEAFNAETFTFHADITLSEKERQIKQOTALVELVKHK 536
 DB 501 CTSSYANRRPCFSSLVVDYVVPFSDDKFIFHKDLCAQGVVALQTMKQEFLLNLVKQK 560
 QY 537 PKATKEQLKAVMDDFAAFEVKCKKADDKETCFABEKGKLVAAQALGL 585
 DB 561 PQITEQLEAVIADFSGLEKCKCQEQEVCFAEEGQKLISKTRALGV 609

Search completed: April 24, 2003, 07:22:43

Job time : 16 secs


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Db 145 EAMCTSPQENAVTFMGHYLHEVARRHPYFYAPELLYAEKYSALIMTECCGADKAACITP 204
Qy 181 KLDELDRDEGKASSAKQRLKASLQKFGRAFAKAWAVARLSQRFPAKAEVSKLVTOLTK 240
Db 205 KLDALKKALASSNQRLKCSLQKFGORAFKANAVARMSQKFPKADFAEITKLATDLTK 264
Qy 241 VHTCCCHGDLLECCADRADLAKYICENODSISLKECEKPLLEKSHCHIAEVENDEMPA 300
Db 265 LTECCCHGDLLECCADRAELAKYICENQASISLQACCDKPVLSKSHCLSEVENDDLPA 324
Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVLLLRKATYETLEK 360
Db 325 DLPSLAADFVEDKECKNYAEAKDVFLGTFLYFYARRHPDYSVALLLRKATYETLEK 384
Qy 361 CAADAPHECAKVFDEKPLVEEPQNLKQNCFLPEOLGEYKFNALLVRYTKVPQVST 420
Db 385 CAEADPSACYKVLDELQPLVEEPKLVKNCFLPEKFLGEGFNALLVRYTKQAPQVST 444
Qy 421 PTLVEVSRNLGKVGSKCKHPKAPCAEDYLSVNLQNLVLEHKTVPVSDRVTKCCTES 480
Db 445 PTLVEAARNLGVKSGKCVLPQALPCVEDYISAILNRVCLVLEHKTVPVSEQVTKCCTGS 504
Qy 481 LVNRRPCFSALEVDVETVYVPEFNAETTFHADICTLSEKEROIKKQALVELVKKPKAT 540
Db 505 VVERRRPCFSALEVDVETVYVPEFNAETTFHADICTLSEKEROIKKQALVELVKKPKAT 564
Qy 541 KEOLKAVMDDFAAAEVKECKKADKTCFAEERGKLVAAASQAAL 583
Db 565 GPQLRTVLGTEATFLDKCCRAEDKEACEFSEGGPKLVASSQAAL 607

RESULT 2
Q8UW05 ID Q8UW05 PRELIMINARY; PRT; 626 AA.
AC Q8UW05;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Ambystoma maculatum (spotted salamander).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC Ambystoma.
OX NCBI_TaxID=43114;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Haverfield E.V., Uzzell T., Spolsky C.M., Bazartseren B.;
RT "Serum albumin of the mole salamanders Ambystoma maculatum and Ambystoma texanum."
RL EMBL: AF217183; AAL56646.1;
DR InterPro: IPR000264; Serum_albumin.
DR Pfam: PF00273; transport_prot; 3.
DR PRINTS: PR00802; SERUMALBUMIN.
DR ProDom: PD002486; Serum_albumin; 1.
DR SMART: SM00103; ALBUMIN; 3.
DR PROSITE: PS00212; ALBUMIN; UNKNOWN_2.
KW Signal.
FT SIGNAL.
FT CHAIN 1 24 POTENTIAL.
SQ SEQUENCE 626 AA; 9D66F57F174AC23F CRC64;

Query Match 40.0%; Score 1242; DB 13; Length 626;
Best Local Similarity 40.1%; Pred. No. 1e-86;
Matches 237; Conservative 110; Mismatches 238; Indels 6; Gaps 3;

Qy 1 DAKHSEVAHRFKDL----GGENFKALVLIAPQYLOQCPFDHVKLVNEYTEFAKTCVAD 56
Db 28 EGHVDNPPLHIGDLIPMIGVDNSKGLVLAAYSQLPLCPYEELHQRVEDVWQIADLCAKG 87
Qy 57 ESEBNCDSLHTLFGDKLCTVATLRETYGEMADCCAKQEPNERCEFLQHKDDN-PNLRL 115

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Db 88 ARHANCAKSPMTIILDELCKKPKNAEKYFPHQECCKEDPERHHCVEHKMANHELTKY 147
Qy 116 VRPEVDVMTAFHDENEETFLKKYLYETARRHPYFAPPELLFAKRYKAAFTTECCQAADKA 175
Db 148 VRPAEQICDKDHAENRGPLLIARYIFMLAIGHPHMYIPAILGFAQRFQDGVSHCKCKDVETA 207
Qy 176 A-CULLPKLDELDRDEGKASSAKQRLKASLQKFGRAFAKAWAVARLSQRFPAKAEVSKL 234
Db 208 GOCFENDKMPHEKHQEVVEYCALQKHCNYILQDFKERALTAYKAVOASQKFFPLASENQI 267
Qy 235 VTDLTKVHTTECHGDLLECCADRADLAKYICENODSISLKECEKPLLEKSHCHIAEVE 294
Db 268 VPDVTVHLHQTCGCGMMACMLERMKLTAKICEKKDELATHLKECCDKPLLSACIIRLP 327
Qy 295 NDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVLLLRKATY 354
Db 328 NDQPADLSPKVPHYIDDPEVKLYTEGGDTFMGRFLYECARRHODYSPEMLRMGSGYE 387
Qy 355 TTLEKCAAADPHCEYAKVFDEKPLVEEPQNLKQNCFLPEOLGEYKFNALLVRYTKK 414
Db 388 EFLKCCAAEGHNECLAkteESLKEESSVTLLKTCGALDKLSYLFQNLILFKYVAR 447
Qy 415 VPQVSTPTLVEVSRNLGKVGSKCKHPKAPCAEDYLSVNLQNLVLEHKTVPVSDRV 474
Db 448 MPALSEQSLRLITKSMTTIGCKCHRPEDQDMTCSEGLGIVFGQICMKQKQKTPVNEKVA 507
Qy 475 KCCTESLVNRRPCFSALEVDVETVYVPEFNAETTFHADICTLSEKEROIKKQALVELV 534
Db 508 QCCSHLSQTSQTPCFSALEVDVETVYVPPPLSVASFNENDELCTTSEPEQSKQVFLIRLMK 567
Qy 535 HKPKATKEQLKAVMDDFAAAEVKECKKADKTCFAEERGKLVAAASQAALGL 585
Db 568 QYPHMTDEQLKTCVNVFVPMVDQCCKADNINECEALEGAKLIDACKAILAV 618

RESULT 3
Q8UW06 ID Q8UW06 PRELIMINARY; PRT; 624 AA.
AC Q8UW06;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Ambystoma texanum (Smallmouth salamander).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC Ambystoma.
OX NCBI_TaxID=8304;
RN [1]
RP SEQUENCE FROM N.A.
RA Haverfield E.V., Uzzell T., Spolsky C.M., Bazartseren B.;
RT "Serum albumin of the mole salamanders Ambystoma maculatum and Ambystoma texanum."
RL EMBL: AF217182; AAL56645.1;
DR InterPro: IPR000264; Serum_albumin.
DR Pfam: PF00273; transport_prot; 3.
DR ProDom: PD002486; Serum_albumin; 1.
DR SMART: SM00103; ALBUMIN; 3.
DR PROSITE: PS00212; ALBUMIN; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 24 POTENTIAL.
SQ SEQUENCE 624 AA; 70321 MW; DE08533BF4953EF7 CRC64;

Query Match 35.0%; Score 1087; DB 13; Length 624;
Best Local Similarity 37.7%; Pred. No. 7.1e-75;
Matches 214; Conservative 102; Mismatches 240; Indels 12; Gaps 5;

Qy 14 LGGENFKALVLIAPQYLOQCPFDHVKLVNEYTEFAKTCVADSEBNCDSLHTLFGDK 73

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Db 45 IGVEHAKALAMALFQMLSKCPHHEQVQRVNVMDIADLCRGAKHGDCGKSVMTIILNE 104
 QY 74 LCTVATLRETYGEMADCCAKQSPERNECFLOHKDDNP-NLPRLVREVDVMTAFDNEE 132
 Db 105 ICKTPENPKYFPHCECKCKEDPERHKCFIEHKSTDPKERTKTEYVKKPSPOICKDHAENRD 164
 QY 133 TELKKYLYEIARRHPFYFAPPELLFFAKRYKAAFTCCQ-AAKAAACLLPKLDELDEGRKA 191
 Db 165 EFLGHVIHKVASSHTTMYPAILSFTLHFDGIVSHCCKDEATVGQCLSEKMPAHKEVEH 224
 QY 192 SSKAKQLKASLOKCFERAFKAWARLRSORPPKAEFAEVSKLVTDLTKVHCECHGDL 251
 Db 225 VCAYOKHNCYILQNFNERALRASAKAHAGCKFFHASFENVRQLTDGIVLHOTHOTCCGDDMM 284
 QY 252 ECADDRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPADLPSLAADFVE 311
 Db 285 ACMAERKLTQTCEK-----KCCCKPVLSECEIVRPNDEKPADLSPVEVRYFD 336
 QY 312 SKDVCKNYAEAKDVFGLMFLEYARRHPDYSVVLRLRLAKTYETTTLEKCCAAADPHECYA 371
 Db 337 DPEVCKRPKEEGDAPMGRFLCDYAKTHPEHSAELNRIASGLEKAYKTCAGAHNECIA 396
 QY 372 KYFDEKPLVEBPONLIKONCELFQOLGEYKFNALLVRYTKYPOVSTPTLVEVSRNLG 431
 Db 397 KEETLRHIEASKTKLTTCGALEKLGYPHFQNMIVRYTGILPRSSDAFLYITKLT 456
 QY 432 KYGSKCKHPEAKRMPCAEDYLSVNLQCLVLEKTPV-SDRVTKCCTESLVNRRPCFSA 490
 Db 457 NIGQCKCKLPEDQOMPSCGGGLGWPAQIC-QNOKTFFENEKLAHCKOSLSFTTTCFRAA 515
 QY 491 LEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKPKATKEOLKAVMD 550
 Db 516 LTVDITYVPAPVTAESFNENDEFTSEADLOAKQKQTFMLHVLVTRHPKITDEQVKITSEK 575
 QY 551 FFAFVEKCKCKADKTCFRAEKGKLVAA 578
 Db 576 FLAMGQCKCKADORNECFATEGAKLVEA 603

RESULT 4

QYXGH6 ID QYXGH6 PRELIMINARY; PRT; 603 AA.
 AC QYXGH6;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Serum albumin precursor (Fragment).
 GN ALB.
 OS Rana shqiperica.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCBI_TaxID=44326;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BUSHAT; TISSUE=LIVER;
 RA Uzzell T., Hotz H.;
 RT "Albumin cDNA sequence of Rana shqiperica: evolutionary changes in
 frog albumins";
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U40452; AAD09338.1; -;
 DR HSSP; P02768; 1E7B.
 DR InterPro; IPR000264; Serum albumin.
 DR Pfam; PF00273; transport_prot; 3.
 DR PRINTS; PR00802; SERUMALBUMIN.
 DR ProDom; PD002486; Serum albumin; 1.
 DR SMART; SM00103; ALBUMIN; 3.
 DR PROSITE; PS00212; ALBUMIN; 3.
 KW Signal.
 ET NON-TER 1 1
 FT SIGNAL <1 23 POTENTIAL.
 FT CHAIN 24 603 SERUM ALBUMIN.
 SQ SEQUENCE 603 AA; 69293 MW; 340D3723FA010C99 CRG64;

Query Match 30.8%; Score 955; DB 13; Length 603;
 Best Local Similarity 33.6%; Pred. No. 8.3e-65;
 Matches 190; Conservative 119; Mismatches 241; Indels 16; Gaps 3;
 QY 12 KDLGENFALVLIAPAYLQOQCPFDHVKLVNEVTEFAKTCVADESAENCDKSLHTFLG 71
 Db 37 KAVGKPAVEKLVLMVAQDFEKGSLDEHLKVQAKIIEAVDNCCKHPEAECKPAIELYH 96
 QY 72 DKLCITVATLRETYGEMADCCAKQSPERNECFLOHKDDNP-LPRLV-----PEVDVMTCT 125
 Db 97 DIVKEEDIDQLYPWMTTECGKAEARTKCFYEHRE-----VRVEEYKIPNIEESCK 148
 QY 126 AFHDNETFLKKYLYEIARRHPFYFAPPELLFFAKRYKAAFTCCQAAADKAAACLLPKLDEL 185
 Db 149 EHKEHPQAFSYLSNIARHSHKLYPPAVLGFAIQYNEITTECCAADKACGGERMPQV 208
 QY 186 RDEGKASSAKQRLKASLOKCFERAFKAWARLRSORPPKAEFAEVSKLVTDLTKVHTEC 245
 Db 209 KKLNTNLEDKHKQKCRVLKEFFERVSQLTLVQVSQRFNGAKYDDVEKVTIEIAHLNEDC 268
 QY 246 CHGDLLECADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPADLPSL 305
 Db 269 CKGDVAVECMTERMEATEHICLAKEKLSKSCCAKGVLETPCILALPNEE--PDLP 326
 QY 306 AADFEVSKDVCKNYAEAKDVFGLMFLEYARRHPDYSVVLRLRLAKTYETTTLEKCCAAAD 365
 Db 327 LKEYEYEDHVCENYQDKRKYLAHFTDYSRSHQESSPOSCLRVSRGFEMLEKCCASAN 386
 QY 366 PHECYAKVDFEPLVEBPONLIKONCELFQOLGEYKFNALLVRYTKYPOVSTPTLVE 425
 Db 387 SAECLEKADAPKLEAALKENEIEISKNGCALEKLGFDNFYQLLVRYFGKMPQVTAQTLVE 446
 QY 426 VSRNLKGVSKCKHPEAKRMPCAEDYLSVNLQCLVLEKTPVSDRVTKCCTESLVNRR 485
 Db 447 LTRMAKIGYVCCGLPDNKKQPCAEKLDILGEMCBREKRTFINDNVHCCVDVSYANRR 506
 QY 486 PCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKPKATKEOLK 545
 Db 507 PCFTKLGYPANYEAPVWDESKLHFTADMKCGSADDQLTKLVLLVEFLKMKPTCGKEKLT 566
 QY 546 AVMDDFAAVFEKCKCKADKTCFRAEE 571
 Db 567 EVIESFRKTVVECCAAENQACFDEK 592

RESULT 5

QY1134 ID QY1134 PRELIMINARY; PRT; 614 AA.
 AC QY1134;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Cobra serum albumin.
 OS Naja naja (Indian cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Naja.
 OX NCBI_TaxID=35670;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=96145734; PubMed=8561913;
 RA Wang X., Hansen H., Havsteen B.;
 RT "Evidence of the coevolution of snake toxin and its endogenous
 antitoxin. Cloning, sequence and expression of a serum albumin cDNA of
 the Chinese cobra";
 RL Biol. Chem. Hoppe-Seyler 376:545-553(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=93343893; PubMed=8343135;
 RA Shao J., Shen H., Havsteen B.;
 RT "Purification, characterization and binding interactions of the


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QY 4 KSEVAHRFKDLGEEFNKALVLIHFAQYLOQCPFEDHVKLVNEVTEFAKTCVADESAENC 63
Db 26 RDKVQOEKTKGDDFRAMTLTMSKFNESFTEISHLVHEMVSLAETCCAGVDPSCY 85
QY 64 KSLHLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVPRVEVDYM 123
Db 86 DTGSSALSAKSCSPDPPFAHPTGAACCLHQGLEOKLCLAALEHPHPPQLPHYVEPVSNEEL 145
QY 124 CTAFFHNEETFLKKLYETARRHPFYAPPELLFFFAKRYKAATTECCQAADKAACLLPKLD 183
Db 146 CEAFKDKPDAFDRFELHEVSSYGQAPLVLGSTRNFLSMVSTCCISPSPTVCFKKEKL 205
QY 184 ELRDEGKASSAKORLKASLOKFGERAFAKAWARLSQRFPKAEFAEVSCLVTDLTVKHT 243
Db 206 ORKTLISLTLMSNR-ACSLAAAYGDKMKFSLYTLMLAQIPASPEDLSPLAEDAAEMFS 264
QY 244 ECCHGDLLECCADR-ADLAKYICENQDSISSKLEKCEC-KPLEKSHCIAEVENDEMPAD 301
Db 265 QCCDSVAEDCIQKLEHTEHTKICATLSAKDKRFADCCCEGKNYQNYFCISSLQPAVAP-K 323
QY 302 LPSLAADFVESDKVCKNYAEAKDVLGMLFLEYARRHPDYSVVLLRLAKTYETTTLEKCC 361
Db 324 LPELOKP--TNKQLCDNCA---LHTRRYMFEARHTNVPDVFGLKYDASENVIKECC 378
QY 362 AAADPHECY----AKVDFEKLVEEPQNLIKONCELFQOLGEYKFNAL--LVRYTKV 415
Db 379 SAKDASSCLDGKROQMGTLPALFLEKTDLQ-----CQYTELNFDFKKRLRDSIROTR-- 432
QY 416 PQVSTPTLVEVSRNLGKVGSKCC 438
Db 433 PDASPELTLQTLQDRADFASCTCC 455

RESULT 8
Q9CY31
ID Q9CY31 PRELIMINARY; PRT; 476 AA.
AC Q9CY31;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Group specific component.
GN GC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC LIVER;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I.,
RA Saio T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cdna collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK010965; BAB27297.1; -.
DR MGD; MGI:95669; Gc.
DR InterPro; IPR000264; Serum_albumin.
```

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DR Pfam; PF00273; transport_prot; 2.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 2.
DR PROSITE; PS00212; ALBUMIN; 1.
SQ SEQUENCE 476 AA; 53614 MW; 11F2EB7FA2B0699 CRC64;

Query Match 12.0%; Score 373; DB 11; Length 476;
Best Local Similarity 24.3%; Pred. No. 1.9e-20;
Matches 111; Conservative 76; Mismatches 226; Indels 44; Gaps 11;

QY 1 DAHSEVAHRFKDLGEEFNKALVLIHFAQYLOQCPFEDHVKLVNEVTEFAKTCVADESAE 60
Db 22 DYEEKVKVCNELAMLGKEDFRSLILYSRKFSSTEQVNQLVKEVSVLSTECCAGADP 81
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVPRVEV 120
Db 82 TCYDTRTSELVSKSCSDAPFPVHPGTPECTKEGLERKLCMAALSHQPOEFTTYVEPTN 141
QY 121 DVNCTAFHNEETFLKKLYETARRHPFYAPPELLFFFAKRYKAATTECCQAADKAACLLP 180
Db 142 DEICEAFRDPKGFADFLYEYSSNYGOAPLPLLVAYTKNLSWVGSCCTSANPTVCVFK 201
QY 181 KIDEURDEGKASSAKORLKASLOKFGERAFAKAWARLSQRFPKAEFAEVSCLVTDLTJK 240
Db 202 ERLQMKHLISLTLTMSNRV-CSQYAAAYGKEKSRSLSHLILKLAQKVPTAKLENVPLAEDFTE 260
QY 241 VITECHGDLLECC-ADDRADLAKYICENQDSISSKLEKCECKPPLLEKSHCIAEVENDEM- 298
Db 261 ILSRCCSTSEDCMASLPEHTIKICQNLKSKNSKEBECQ-----ENTPMN 307
QY 299 -----PADLPSLAADFVESKDYC-KNYAEAKDVLGMLFLEYARRHPDYSVVL 345
Db 308 IFMCTYFMPAAEPQLP--AIKLPTGKDLGCGSTTQAMD----QYTFELSRRTQVEVFL 361
QY 346 LLRLAKTYETTTLEKCCAAADPHECYAKVDFEKLVE-EPQNLIKONCELFQOLGEYKFP- 403
Db 362 SKVLEPTLK-TLRECCDQDSVAC----FSTQSPLLKRLQLTSPFERQEMCADYSENTFT 416
QY 404 --QNALLVRYTKVPOVSTPTLVEVSRNLGKVGSKCC 438
Db 417 EYKKLAERLRTKTPNTSPAELKDMVEKHSDFASKCC 453

RESULT 9
Q91XG1
ID Q91XG1 PRELIMINARY; PRT; 476 AA.
AC Q91XG1;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Group specific component.
GN GC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010762; AAH10762.1; -.
DR MGD; MGI:95669; Gc.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 2.
DR ProDom; PD002486; Serum_albumin; 1.
DR PROSITE; PS00212; ALBUMIN; UNKNOWN 1.
SQ SEQUENCE 476 AA; 53600 MW; 633B0CE183CD43FD CRC64;

Query Match 12.0%; Score 372; DB 11; Length 476;
Best Local Similarity 24.3%; Pred. No. 2.3e-20;
Matches 111; Conservative 75; Mismatches 227; Indels 44; Gaps 11;
```



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FT  NON_TER      1
PT  NON_TER      123
SQ  SEQUENCE      123 AA; 13824 MW; B18F83BC2E14F29 CRC64;

Query Match          9.3%; Score 290; DB 13; Length 123;
Best Local Similarity 43.0%; Pred.No. 8.2e-15;
Matches 52; Conservative 22; Mismatches 47; Indels 0; Gaps

Qy  452 YLSVVLNQLCVLHEKTPVSDRVTKCCTPESLVNRRPCFSALEVDVETVYPKEFNAETTFHA 571
      |||:: :| |||::|::|:: :|||::| :||| :| :|
Db   1 YLTVIIEDMCKQESTPVNDQVSQCCNDLYSDKRPCFTAMGTDTKYVPPADPTLFDFFE 60

Qy  512 DICTLSKERQIKQTALVELVHKHKPATVEQLKAVNMDFAAFVEKCKCKADDDKTCFAEE 571
      |||::|::| :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   61 KMKCAPPAEREAGELKLLVNLVRRKPKQMTBEQLKKITEGFTAMMECKCKKPDVEGCLGEE 120

Qy  572 G 572
Db   121 G 121

RESULT 13
ID  Q63205 PRELIMINARY; PRT; 135 AA.
AC  Q63205;
DT  01-NOV-1996 (TremBLrel. 01, Created)
DT  01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT  01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE  Messenger RNA for rat alpha-fetoprotein (Fragment).
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]

```

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RP SEQUENCE FROM N.A.
RX MEDLINE=81006964; PubMed=6157690;
RT "Inis M.A., Miller D.L.;
RA "Alpha-fetoprotein gene expression. Partial DNA sequence and COOH-
RT terminal homology to albumin."
RL J. Biol. Chem. 255:8994-8996(1980).
DR EMBL; V01236; CAA24546.1; -.
DR HSSP; P02768; IE7B.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 1.
DR SMART; SM00103; ALBUMIN; 1.
FT NON_TER 1
SQ SEQUENCE 135 AA; 15040 MW; 0F922DAF4F71EAC4 CRC64;

Query Match 8.5%; Score 264; DB 11; Length 135;
Best Local Similarity 41.0%; Pred No. 8 9e-13;

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Qy    450 EDYLSVVLNOLCVLHKEITVPVSDRVTKCTESLVNRRCFSALEVEDYETIVPKFEANAFTTF 509
      | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db    1 EGLADIIVIGHLCRLHEANPVNSGINHCSSSYSNRRUCITSFLRDEITYVPLPFSATNSSS 60

Qy    510 HADICTILSEKEROIKQTALVELVKHKPKATKEQLKAVMDDEAFAYVEKCKCADDKETCPA 569
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db    61 TRNLCOAGRAPQMKGELLINLVKQAPEMTEEOHAHVTAADFSGLLKKCRKDODDCAFA 120

Qy    570 EE 571
      : |
Db    121 KE 122

RESULT 14
QJUMX8 PRELIMINARY; PRT; 1723 AA.
AC QJUMX8
DT 01-OCT-2000 (TtEMBLrel. 15, Created)
DT 01-OCT-2000 (TtEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TtEMBLrel. 15, Last annotation update)
DE Cag-y.
```

GN CAG-Y.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CCUG 17874;
 RX MEDLINE=97121442; PubMed=8962108;
 RA Censini S., Lange C., Xiang Z., Crabtree J.E., Ghiara P.,
 Borodovsky M., Rappuoli R., Covacci A.;
 RT "cag, a pathogenicity island of Helicobacter pylori, encodes type I-
 specific and disease-associated virulence factors";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14648-14653(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CCUG 17874;
 RX MEDLINE=20150112; PubMed=10684850;
 RA Covacci A., Rappuoli R.;
 RT "Tyrosine-phosphorylated bacterial proteins: Trojan horses for the
 RT host cell";
 RL J. Exp. Med. 191:587-592(2000).
 DR EMBL; AF282852; AAF80198.1; -;
 SQ SEQUENCE 1723 AA; 196048 MW; 0FAC456B76622801 CRC64;

 Query Match 6.1%; Score 188; DB 2; Length 1723;
 Best Local Similarity 22.9%; Pred. No. 1.2e-05;
 Matches 157; Conservative 88; Mismatches 254; Indels 188; Gaps 37;

 QY 16 EENFKALVLIAPAYIQQCPFFDHVKLVNEVTEFAKTCVADESAENC-----DKSLHTLF 70
 DB 351 EERIKLDLIKDNKLLKSLNQKQVQVALDCLKNKNT---DEBRNECLKLINDPEIREKF 407

 QY 71 GDLCTVATLRETYGEMADCC--AKOEPERNECFLOHKDDNPMLPRLVRPEVDVMTAFH 128
 DB 408 RKEL----GLQELQYKDCIKNAKTEAEKNECKLSKE--AIERLKQOALDCLKNKNT 461

 QY 129 DNEETFLKLYEIAIRHPYFYAPELL--FFAKRYKAAFTCCQAADKAAC---LLPK 181
 DB 462 DEERN-----ECLKNIPQDLQKELLADMSVKAYKDCVSRARNEKEKECEKLLTPEAR 514

 QY 182 -----LDELREGKASAKQRLKAS-----LQKGERAFKAWAVARLSQRP 224
 DB 515 KLEQOVLQCLKN---AKTDEERKCKLDLPKDLQSDILAKESLKAYKDC---VSQAKT 567

 QY 225 KAEFAEVSILVT-----DLTKVHTEC-----CHGDLLECADRADL 260
 DB 568 EAEKKECEKLLTPEAKKLLLEBAKESVKAYLDCVSOAKTEAEKKECEKLLTPEAKKLEB 627

 QY 261 AK-----YI-CENQDSISSKLEKCE-----KPLLEKS--HCI--AEVEND-----EM 298
 DB 628 AKKSVKAYLDCVSOAKTEDEKKECEKLLTPEAKKLLLEQOALDCLKNKNTADKRCVKDL 687

 QY 299 PADLPS--LAAD-----FVSKDVCKNYAEAKOVFLGMFLYEVARRHPDYSVVLNLLAKT 352
 DB 688 PKDLQKVLAKESVRYLYLDCVSRARNEKE--CEKLLTPEAK-----LLEAKK 737

 QY 353 YETLEKCCAAA-----DPHECYAKVDFEPLVEEPQNLKQNCLEFQOL---GEYKFN 405
 DB 738 SVKAYKDCVSRARNEKEKECEKLLTPEAKKLLLEBAKESVKAYLDCVSOAKTEDEKKECE 797

 QY 406 ALVRYTKKVPQVSTPTLVE---VSRNLGKVGSKCKH---PEAKRMPCAEDYLSVNLN 458
 DB 798 KLLTPEAKKLLLEBAKESVKAYLDCVSOAKTEDEKKECEKLLTPEAKL-----LE 847

 QY 459 QL----CVLHEKTPVSDRVTKCTESLVNRRPCFSALEVDYTPKFEFNAETFT-----FH 510
 DB 848 QOALDCLKNKNTAD---KKRCVKDL-----PKDLQKVLAKKSVKAY 887

 QY 511 ADICITLSEKQIKK--QTALVELVHKHPKATKEQLKAVMDDFAAFVEKCKCKADDDKTC--- 567
 DB 888 LDCVSRARNEKEKECEKLLTPEAKKLLLEBAKESLKAYKD---CLSQARNEEERACEK 943

QY 568 -----FAEKGKLVAA-----SQA 581
 DB 944 LLTPEARKLLEAKSKVKAYLDCVSOA 970

 RESULT 15
 Q9ZLVO PRELIMINARY; PRT; 1819 AA.
 AC Q9ZLVO;
 DT 01-MAY-1999 (TREMELrel. 10, Created)
 DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
 DE 01-MAR-2002 (TREMELrel. 20, Last annotation update)
 DE CAG island protein.
 GN JHP0476.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=85963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 Smith D.R., Noonan B., Gullid B.C., deJonge B.L., Carmel G.,
 Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen Helicobacter pylori";
 RL Nature 397:176-180(1999).
 DR EMBL; AE001481; AAD06047.1; -;
 KW Complete proteome.
 SQ SEQUENCE 1819 AA; 207505 MW; E76762B5A7FA371D CRC64;

 Query Match 5.9%; Score 184; DB 16; Length 1819;
 Best Local Similarity 21.8%; Pred. No. 2.7e-05;
 Matches 150; Conservative 101; Mismatches 278; Indels 158; Gaps 34;

 QY 16 EENFKALVLIAPAYIQQCPFFDHVKLVNEVTEFAKTCVADESAENC-----DKSLHTLF 70
 DB 371 EERIKLDLIKDNKLLKSLNQKQVQVALDCLKNKNT---DEBRNECLKLINDPEIREKF 427

 QY 71 GDLCTVATLRETYGEMADCC--AKOEPERNECFLOHKDDNPMLPRLVRPEVDVMTAFH 128
 DB 428 RKEL----GLQELQYKDCIKNAKTEAEKNECKLSKE--AIERLKQOALDCLKNKNT 481

 QY 129 DNEETFLKLYEIAIRHPYFYAPELL--FFAKRYKAAFTCCQAADKAAC---LLPKLD 183
 DB 482 DEERK-----ECLKNIPQDLQKELLADMSVKAYKDCVSRARNEKEKECEKLLTPEAK 534

 QY 184 ELRDE-----GKASSAKQRLKAS-----LQKGERAFKAWAVARLSQRPKAE 227
 DB 535 KLEENQALDCLKNKNTDEERKCKLNLPKDLQSDILAKESLKAYKDC---SQAKTEAE 590

 QY 228 FAEVSKLVT-----DLTKVHTEC-----CHGDLLECADRADLAK- 262
 DB 591 KKECEKLLTPEAKKLLLEBAKESVKAYLDCVSOAKTEAEKKECEKLLTPEAKKLEAK 650

 QY 263 -----YI-CENQDSISSKLEKCE-----KPLLEKS--HCIAEVEND-----MPAD 301
 DB 651 SVRAYLDCVSRARNEKEKECEKLLTPEAKKLLLEBAKESVKAYLDCVSOAKTEAEKKECEK 710

 QY 302 LPS-----FVSKDVCKNYAEAKOVFLGMFLYEVARRHPDYSVVLNLLAKTYET 355
 DB 711 LQKVLAKESVRYLYLDCVSRARNEKE--CEKLLTPEAK-----LLEAKSKVK 760

 QY 356 TLEKCCAAA-----DPHECYAKVDFEPLVEEPQNLKQNCLEFQOL---GEYKFNALL 408
 DB 761 AYKDCVLRARNEKEKECEKLLTPEAKKLLLEBAKESVKAYLDCVSKAKNAEAKKECEKLL 820

 QY 409 VRYTKKVPQVSTPTL-----VEVSRNLGKVGSKCKC--HPEAKRMPCAEDYLSVNLNQL 460
 DB 821 TPEARKLLEBAKESVKAYKDCVSRARN--BKEQKECEKLLTPEARKL--LEESKSKVAYLD 878

QY 461 CVLHEK-----TPVSDRVTKCTESLVNRRPCFSAL-----EVDETYVPKE 501
Db 879 CVSKAKNEAEKECEKLLTPEARKLLEAKESVKAYKDCVSRARNEKEKECEKLLTPE- 937
QY 502 FNAETFTFHADICTLSEKERQIKOTALVELVK--HKPKATKEQLKAVMDDFAAFVEKCC 559
Db 938 --AKLLENQALDCLKNAKTEAEKRRCKVDLPKDLQKVLAKESVRVYLD----CVSKAK 991
QY 560 KADDKETC---FAEGGKLVAAASQAAL 583
Db 992 NEAEKECEKLLTPEARKLLEAKESV 1018

Search completed: April 24, 2003, 07:24:00
Job time : 44 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 24, 2003, 07:22:19 ; Search time 77 seconds
(without alignments)
1012.359 Million cell updates/sec

Title: US-09-833-111-18

Perfect score: 3103

Sequence: 1 DAHSEVAHREKDLGLENFK.....TCFAEGKKLVAASQAALGL 585

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_101002.*

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- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3103	100.0	585	10 AAP90388	Mature human serum
2	3103	100.0	585	11 AAR05318	Human serum albumin
3	3103	100.0	585	11 AAR06457	Human serum albumin
4	3103	100.0	585	16 AAR0301	Human serum albumin
5	3103	100.0	585	18 AAO20111	HSA protein sequen
6	3103	100.0	585	21 AAY84873	Amino acid sequenc
7	3103	100.0	585	21 AAY83946	Yeast codon-biased
8	3103	100.0	585	22 ABB79006	Human mature album
9	3103	100.0	585	22 AAE13399	Human albumin (HA)
10	3103	100.0	585	22 AAM52567	Mature human serum

11	3103	100.0	585	22 AAE13129	Human albumin (HA)
12	3103	100.0	585	22 AAE12403	Human albumin (HA)
13	3103	100.0	585	22 AAE08578	Human serum albumi
14	3103	100.0	585	23 ABG63321	Human serum albumi
15	3103	100.0	585	23 ABJ00986	B lymphocyte stimu
16	3103	100.0	585	23 ABG33847	Human B lymphocyte
17	3103	100.0	585	23 AAU75220	Mature form of hum
18	3103	100.0	609	21 AAB36542	Recombinant human
19	3103	100.0	609	21 AAB36549	Recombinant human
20	3103	100.0	609	21 AAY78147	Pre human serum al
21	3103	100.0	610	14 AAR39510	Chimeric human ser
22	3103	100.0	670	21 AAB36543	Recombinant human
23	3103	100.0	670	21 AAB36550	Recombinant human
24	3103	100.0	783	14 AAR39473	Prepro-HSA-G-CSF c
25	3103	100.0	787	14 AAR39477	G-CSF-(Gly)4-HSA c
26	3103	100.0	853	14 AAR39472	Sequence of mature
27	3099	99.9	585	10 AAP93344	Sequence of mature
28	3099	99.9	585	19 AAP59841	Mature protein of
29	3099	99.9	608	17 AAR96229	Human serum albumi
30	3099	99.9	609	4 AAP30089	Sequence of human
31	3099	99.9	609	17 AAR96232	Human serum albumi
32	3099	99.9	609	17 AAR94572	Cancer metastasis
33	3099	99.9	609	17 AAR88913	Human serum albumi
34	3099	99.9	609	19 AAW48095	Human serum albumi
35	3099	99.9	609	20 AAY06994	Human albumin. Ho
36	3099	99.9	609	22 AAB04148	Myosin light chain
37	3097	99.8	779	18 AAW22719	Human serum albumi
38	3097	99.8	784	18 AAW22717	Human serum albumi
39	3097	99.8	789	18 AAW22718	Human serum albumi
40	3097	99.8	794	18 AAW22720	Human serum albumi
41	3096	99.8	609	7 AAP60092	Sequence of prepro
42	3095	99.7	586	8 AAP70767	Human serum albumi
43	3095	99.7	609	13 AAR25309	HSA. Pichia pasto
44	3095	99.7	754	17 AAR92149	HSA:Fc gamma RII f
45	3095	99.7	978	19 AAW48096	Human serum albumi

ALIGNMENTS

RESULT 1

AAP90388

ID AAP90388 standard; protein; 585 AA.

XX

AC AAP90388;

XX

DT 01-NOV-1989 (first entry)

XX

DE Mature human serum albumin polypeptide.

XX

KW Human serum albumin; mature protein; new polypeptides;

XX

KW plasma expanders.

XX

OS Homo sapiens (Human).

XX

PN EP322094-A.

XX

PD 28-JUN-1989.

XX

PF 25-OCT-1988; 88EP-0310000.

XX

PR 30-OCT-1987; 87GB-0025529.

XX

PA (DELT) DELTA BIOTECH LTD.

XX

PI Ballance DJ, Hinchliffe E, Geisow MJ, Senior PJ;

XX

DR WPI; 1989-186464/26.

XX

DR N-PSDB; AAN90128.

XX

PT New N-terminal fragments of human serum albumin

XX

PT - esp. useful as blood plasma expanders.

PS Disclosure; fig 2; 20pp; English.

XX Mature protein of human serum albumin (see corresp. AAN90128).
 CC Used to make new N-terminal fragments which are used as plasma
 CC expanders, or as substitutes for HSA or BSA, in tissue culture
 CC media.
 XX
 SQ Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 10; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1e-254;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHRFKDLGGENFKALVLI AFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 60
 DB 1 DAHSEVAHRFKDLGGENFKALVLI AFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 60
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPRNECFLOHKDDNPRLVRPEV 120
 DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPRNECFLOHKDDNPRLVRPEV 120
 QY 121 DVMTAFHNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
 DB 121 DVMTAFHNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
 QY 181 KLDELDEGKASSAKORLKCASLQKGERAFKAWAVARLSORPPKAEFAEVSCLVTDLT 240
 DB 181 KLDELDEGKASSAKORLKCASLQKGERAFKAWAVARLSORPPKAEFAEVSCLVTDLT 240
 QY 241 VHTCECHGDLLECADRADLAKYICENQDSISSKLEKCECKPLEKSHCIAEVENDEMPA 300
 DB 241 VHTCECHGDLLECADRADLAKYICENQDSISSKLEKCECKPLEKSHCIAEVENDEMPA 300
 QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYEYARRHPDYSVLLRLAKTYETTLEK 360
 DB 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYEYARRHPDYSVLLRLAKTYETTLEK 360
 QY 361 CAADPHECYAKVDFEFPKLVPEEPQNLKQNCLEFQGLGEYKFQNALLVRYTKKVPQVST 420
 DB 361 CAADPHECYAKVDFEFPKLVPEEPQNLKQNCLEFQGLGEYKFQNALLVRYTKKVPQVST 420
 QY 421 PTLVEVSRLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCTES 480
 DB 421 PTLVEVSRLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCTES 480
 QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
 DB 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
 QY 541 KEOLKAVMDDFAAFVEKCKCKADDDKTCFAEEGKKLVAAASQAALGL 585
 DB 541 KEOLKAVMDDFAAFVEKCKCKADDDKTCFAEEGKKLVAAASQAALGL 585

RESULT 2
 AAR05318
 ID AAR05318 standard; protein; 585 AA.
 XX
 AC AAR05318;
 DT 08-OCT-1990 (first entry)
 XX
 DE Human serum albumin gene product.
 XX
 KW Human serum albumin; HSA-A; yeast; ds.
 XX
 OS Homo sapiens.
 XX
 PN JP02117384-A.
 XX
 PD 01-MAY-1990.
 XX
 PF 26-OCT-1988; 88JP-0268302.

XX

PR 26-OCT-1988; 88JP-0268302.
 XX (TOFU) TOA NENRYO KOGYO KK.
 PA
 XX WPI; 1990-176228/23.
 DR N-PSDB; AAQ04719.
 DR
 XX
 XX Human serum albumin prepn. by yeast host -
 PT by culturing transformed plasmid yeast to produce serum, and
 PT removing it.
 XX
 PS Disclosure; : pp; Japanese.
 XX
 CC Mature HSA-A may be produced using the sequence incorporated into a
 CC plasmid vector with suitable controllers, and transferred to a yeast
 CC expression system.
 XX

SQ Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 11; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1e-254;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHRFKDLGGENFKALVLI AFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 60
 DB 1 DAHSEVAHRFKDLGGENFKALVLI AFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 60
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPRNECFLOHKDDNPRLVRPEV 120
 DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPRNECFLOHKDDNPRLVRPEV 120
 QY 121 DVMTAFHNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
 DB 121 DVMTAFHNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
 QY 181 KLDELDEGKASSAKORLKCASLQKGERAFKAWAVARLSORPPKAEFAEVSCLVTDLT 240
 DB 181 KLDELDEGKASSAKORLKCASLQKGERAFKAWAVARLSORPPKAEFAEVSCLVTDLT 240
 QY 241 VHTCECHGDLLECADRADLAKYICENQDSISSKLEKCECKPLEKSHCIAEVENDEMPA 300
 DB 241 VHTCECHGDLLECADRADLAKYICENQDSISSKLEKCECKPLEKSHCIAEVENDEMPA 300
 QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYEYARRHPDYSVLLRLAKTYETTLEK 360
 DB 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYEYARRHPDYSVLLRLAKTYETTLEK 360
 QY 361 CAADPHECYAKVDFEFPKLVPEEPQNLKQNCLEFQGLGEYKFQNALLVRYTKKVPQVST 420
 DB 361 CAADPHECYAKVDFEFPKLVPEEPQNLKQNCLEFQGLGEYKFQNALLVRYTKKVPQVST 420
 QY 421 PTLVEVSRLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCTES 480
 DB 421 PTLVEVSRLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCTES 480
 QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
 DB 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
 QY 541 KEOLKAVMDDFAAFVEKCKCKADDDKTCFAEEGKKLVAAASQAALGL 585
 DB 541 KEOLKAVMDDFAAFVEKCKCKADDDKTCFAEEGKKLVAAASQAALGL 585

RESULT 3
 AAR08457
 ID AAR08457 standard; Protein; 585 AA.
 XX
 AC AAR08457;
 XX
 DT 16-APR-1991 (first entry)
 XX

DE Human serum albumin.
 XX HSA; folding; ss.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 123..303.
 FT /label= A
 FT Region 1..303
 FT /label= B
 FT Region 123..585
 FT /label= C
 XX
 PN JP0227079-A.
 XX
 PD 25-AUG-1989.
 XX
 PF 10-SEP-1990; 90JP-0250926.
 XX
 PR 06-OCT-1988; 88JP-0250926.
 XX
 PA (TOFU) TONEN CORP.
 XX
 XX WPI; 1990-317325/42.
 DR N-PSDB; AAQ06099.
 XX
 PT New human serum albumin fragments - used to bond medicines and for
 PT stable folding of protein(s).
 XX
 PS Claim 1; Fig 8; 24pp; Japanese.
 XX
 CC Fragments A-C of HSA are expressed as fusion proteins with the
 CC signal peptide of E. coli alkaline phosphatase. The fragments are
 CC selected for their specific properties. The C-terminal truncated
 CC fragment, B, does not bind long-chain fatty acids but does bind to
 CC various medicines at the central region. The N-terminal truncated
 CC fragment, C, has good stability in protein folding. The central
 CC segment, A, has characteristics of both B and C.
 CC See also AAQ06099-Q06098.
 XX
 SQ Sequence 585 AA;
 Query Match 100.0%; Score 3103; DB 11; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1e-254;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHSEVAHFKDLGEENFKALVLIAPFAQYLQOCPFEDHVKLVNEVTEFAKTCVADESAAE 60
 DB 1 DAHSEVAHFKDLGEENFKALVLIAPFAQYLQOCPFEDHVKLVNEVTEFAKTCVADESAAE 60
 QY 61 NCDKSLHFLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPMLPRLVRPEV 120
 DB 61 NCDKSLHFLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPMLPRLVRPEV 120
 QY 121 DVMTAFHDNETFLKKYLYETARHPYFYAPPELLFFAKRYKAAPTECCQADRAACLLP 180
 DB 121 DVMTAFHDNETFLKKYLYETARHPYFYAPPELLFFAKRYKAAPTECCQADRAACLLP 180
 QY 181 KIDELRDEGKASSAKORLKCSLQKFGFRAFKAWAVARLSQRFPAEFAEYSKLVTDLT 240
 DB 181 KIDELRDEGKASSAKORLKCSLQKFGFRAFKAWAVARLSQRFPAEFAEYSKLVTDLT 240
 QY 241 VHTTECHGDLLECADDRADLAKYICENQDSISSKKECKEPLLEKSHCIAEVENDEMPA 300
 DB 241 VHTTECHGDLLECADDRADLAKYICENQDSISSKKECKEPLLEKSHCIAEVENDEMPA 300
 QY 301 DLPSLAADFVSKOVCKNYAEAKOVFLGMFLYEYARRHPDYSVLLLLAKTYETTLK 360
 DB 301 DLPSLAADFVSKOVCKNYAEAKOVFLGMFLYEYARRHPDYSVLLLLAKTYETTLK 360
 QY 361 CAADPHCEYAKVFDEFKPLVEEPONLIKQNCSELFQGLGEYKFNQALLVRYTKKVPQVST 420
 DB 361 CAADPHCEYAKVFDEFKPLVEEPONLIKQNCSELFQGLGEYKFNQALLVRYTKKVPQVST 420

Db 361 CAADPHCEYAKVFDEFKPLVEEPONLIKQNCSELFQGLGEYKFNQALLVRYTKKVPQVST 420
 QY 421 PTLVEVSRLKGVSKCKCKHPEAKRMPCAEDYLSVVLNQLCVLHKEKTPVSDRVTCKCTES 480
 DB 421 PTLVEVSRLKGVSKCKCKHPEAKRMPCAEDYLSVVLNQLCVLHKEKTPVSDRVTCKCTES 480
 QY 481 LVNRRPCFSALEVDYTPKPEFNAETFTFHADICTLSSEKEROIKKOTALVELVKKHKPRAT 540
 DB 481 LVNRRPCFSALEVDYTPKPEFNAETFTFHADICTLSSEKEROIKKOTALVELVKKHKPRAT 540
 QY 541 KEQLKAVMDFAAFVEKCKKADDKETCFABEGKKLVAAASQAALGL 585
 DB 541 KEQLKAVMDFAAFVEKCKKADDKETCFABEGKKLVAAASQAALGL 585
 RESULT 4
 AAR80301
 ID AAR80301 standard; Protein; 585 AA.
 AC AAR80301;
 XX 17-JAN-1996 (first entry)
 DT Human serum albumin.
 DE
 XX Serum albumin; HSA; aspartyl protease-3; Yap3p;
 KW Saccharomyces cerevisiae.
 XX Homo sapiens.
 OS
 XX WO9523857-A1.
 PN
 XX 08-SEP-1995.
 PD
 XX 01-MAR-1995; 95WO-GB00434.
 PF
 XX 05-MAR-1994; 94GB-0004270.
 PR
 XX (DELZ) DELTA BIOTECHNOLOGY LTD.
 PA
 XX Gilbert SC, Kerry-Williams SM;
 PI
 XX WPI; 1995-320572/41.
 DR N-PSDB; AAQ98695.
 DR
 XX Yeast with reduced levels of aspartyl protease 3 proteolytic
 PT activity - used to secrete human albumin without prodn. of the 45
 PT kD fragment
 XX
 PS Example 1; Page 26-28; 50pp; English.
 XX
 CC The cDNA given in AAQ98695, which encodes HSA (AAR80301), was subjected
 CC to site-directed mutagenesis to investigate the role of
 CC endoproteases in the generation of a 45 kDa albumin fragment obtd.
 CC when the cDNA is expressed in S. cerevisiae. Mutations were: R410A;
 CC L407A, L408V, V409A; and R410A, K413Q, K414Q. The latter set of
 CC mutations, especially, improved stability of HSA to yeast Yap3p
 CC proteolytic cleavage, allowing increased prodn. of recombinant HSA.
 XX
 SQ Sequence 585 AA;
 Query Match 100.0%; Score 3103; DB 16; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1e-254;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHSEVAHFKDLGEENFKALVLIAPFAQYLQOCPFEDHVKLVNEVTEFAKTCVADESAAE 60
 DB 1 DAHSEVAHFKDLGEENFKALVLIAPFAQYLQOCPFEDHVKLVNEVTEFAKTCVADESAAE 60
 QY 61 NCDKSLHFLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPMLPRLVRPEV 120
 DB 61 NCDKSLHFLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPMLPRLVRPEV 120

121 DVMTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
121 DVMTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
181 KLDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLTk 240
181 KLDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLTk 240
241 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPA 300
241 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPA 300
301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYIARRHPDYSVLLLRILAKTYETTTLEK 360
301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYIARRHPDYSVLLLRILAKTYETTTLEK 360
361 CAADPHCEYAKVDFEFPKPLVEEPQNLKQNCBELFQLGGEYKFNALLVRYTKKVPQVST 420
361 CAADPHCEYAKVDFEFPKPLVEEPQNLKQNCBELFQLGGEYKFNALLVRYTKKVPQVST 420
421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHETKTPVSDRYTKCCTES 480
421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHETKTPVSDRYTKCCTES 480
481 LVNRRPCFSALEVDITYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
481 LVNRRPCFSALEVDITYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
541 KEOLKAVMDDDFAAFVEKCKKADKCTCFABEGKKLVAASQAALGL 585
541 KEOLKAVMDDDFAAFVEKCKKADKCTCFABEGKKLVAASQAALGL 585

W097 12-44-15

RESULT 5
AAO20111
ID AAO20111 standard; Protein: 585 AA.
XX AAO20111;
XX AC AAO20111;
XX DT 06-AUG-2002 (first entry)
XX DE HSA protein sequence related to the growth hormone protein.
XX KW Serum albumin-growth hormone fusion protein; growth hormone;
XX KW Down's syndrome.
XX OS Unidentified.
XX PN KR99076789-A.
XX PD 15-OCT-1999.
XX PF 25-JUN-1998; 98RR-0704914.
XX PR 30-DEC-1995; 95GB-0026733.
XX PR 19-DEC-1996; 96WO-GB03164.
XX PA (DELTA) DELTA BIOTECHNOLOGY LTD.
XX DR WPI; 1997-363680/55.
XX DR N-PSDB; AAK99568.
XX PT Serum albumin-growth hormone fusion protein - useful to treat growth
XX PT hormone related diseases, e.g. Down's syndrome
XX PS Disclosure; Fig 6; 21pp; Korean.
XX CC The invention relates to a serum albumin-growth hormone fusion protein -
XX CC useful to treat growth hormone related diseases such as Down's syndrome.
XX CC This sequence represents a HSA protein related to the serum albumin-
XX CC growth hormone protein of the invention.
XX SQ Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 18; Length 585;
Best Local Similarity 100.0%; Pred No. 1e-254;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAHKSEVAHRFKDLGGENFKALVLIAPYQLOCPEDHVKLVNEVTEFAKTCVADESAAE 60
DB 1 DAHKSEVAHRFKDLGGENFKALVLIAPYQLOCPEDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCHVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVLRPEV 120
DB 61 NCDKSLHTLFGDKLCHVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVLRPEV 120
QY 121 DVMTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
DB 121 DVMTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
QY 181 KLDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLTk 240
DB 181 KLDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLTk 240
QY 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPA 300
DB 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPA 300
QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYIARRHPDYSVLLLRILAKTYETTTLEK 360
DB 301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYIARRHPDYSVLLLRILAKTYETTTLEK 360
QY 361 CAADPHCEYAKVDFEFPKPLVEEPQNLKQNCBELFQLGGEYKFNALLVRYTKKVPQVST 420
DB 361 CAADPHCEYAKVDFEFPKPLVEEPQNLKQNCBELFQLGGEYKFNALLVRYTKKVPQVST 420
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHETKTPVSDRYTKCCTES 480
DB 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHETKTPVSDRYTKCCTES 480
QY 481 LVNRRPCFSALEVDITYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
DB 481 LVNRRPCFSALEVDITYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
QY 541 KEOLKAVMDDDFAAFVEKCKKADKCTCFABEGKKLVAASQAALGL 585
DB 541 KEOLKAVMDDDFAAFVEKCKKADKCTCFABEGKKLVAASQAALGL 585
RESULT 6
AAO20111
ID AAO20111 standard; protein: 585 AA.
XX AC AAO20111;
XX DT 08-AUG-2000 (first entry)
XX DE Amino acid sequence of a human albumin protein.
XX KW Human; albumin; ischemic state; serum protein; metal ion salt;
XX KW peroperative ischemia; ischemia; myocardial infarction;
XX KW progressive coronary artery disease.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "optionally acetylated, and claimed under
XX FT claim 56"
XX PN WO200020840-A1.
XX PD 13-APR-2000.
XX PF 01-OCT-1999; 99WO-US22905.
XX SQ

PR 02-OCT-1998; 98US-0102738.
 PR 02-OCT-1998; 98US-0165581.
 PR 02-OCT-1998; 98US-0165926.
 PR 11-JAN-1999; 99US-0115392.
 XX (ISCH-) ISCHEMIA TECHNOLOGIES INC.
 FA
 XX Bar-Or D, Lau E, Winkler JV;
 XX WPI; 2000-303843/26.

XX New method for the continuous detection of ischemic states comprises
 PT detecting and quantifying the existence of an alteration of the serum
 PT protein albumin -
 XX
 XX Disclosure; Page 97-100; 105pp; English.

XX The present sequence represents human albumin protein. The specification
 CC describes a method for the continuous detection of ischemic states. The
 CC method comprises detecting and quantifying the existence of an alteration
 CC of the serum protein albumin. The method comprises contacting a
 CC biological sample containing albumin from the patient with an excess
 CC quantity of a metal ion salt, where the metal ion binds to the N-terminus
 CC of naturally occurring human albumin, to form a mixture containing bound
 CC metal ions and unbound metal ions, and then determining the amount of
 CC metal ions bound to the albumin N-terminus. The amount of bound metal
 CC ions is correlated to a known value to determine the occurrence or
 CC non-occurrence of an ischemic event. The methods are useful for detection
 CC of ischemic states. The methods are also useful for distinguishing
 CC peroperative ischemia from ischemia caused by , amongst other things,
 CC myocardial infarctions and progressive coronary artery disease.

XX Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 21; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1e-254;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHSEVAHREKDLGEENFKALVLIATAFYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 60
 Db 1 DAHSEVAHREKDLGEENFKALVLIATAFYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 60
 Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPRLVRPEV 120
 Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPRLVRPEV 120
 Qy 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
 Db 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
 Qy 181 KLDELDRDEGKASSAKQRLKASLOKFGRAFKAFAVARSORFPAEVSRLVTDLT 240
 Db 181 KLDELDRDEGKASSAKQRLKASLOKFGRAFKAFAVARSORFPAEVSRLVTDLT 240
 Qy 241 VHTCCGDLLECADRADLAKYICENQDSISSKKECCERPLLEKSHCIAEVENDEMPA 300
 Db 241 VHTCCGDLLECADRADLAKYICENQDSISSKKECCERPLLEKSHCIAEVENDEMPA 300
 Qy 301 DLPSLAADFVESKDVCKNYAKADKDFVGMFLYFYARRHPDYSVLLRLAKTYETLEK 360
 Db 301 DLPSLAADFVESKDVCKNYAKADKDFVGMFLYFYARRHPDYSVLLRLAKTYETLEK 360
 Qy 361 CAADPHCEYAKVDFEFPVLEEONLIKQNCFLFEQGLGEYKFNALLVRYTKVPQVST 420
 Db 361 CAADPHCEYAKVDFEFPVLEEONLIKQNCFLFEQGLGEYKFNALLVRYTKVPQVST 420
 Qy 421 PTLVEVSRNLKGVSKCKHPEAKRMPCAEDYLSVNLQNLVLEHKTVPVSRVTKCCTES 480
 Db 421 PTLVEVSRNLKGVSKCKHPEAKRMPCAEDYLSVNLQNLVLEHKTVPVSRVTKCCTES 480
 Qy 481 LVNRRPCFSALEVDYTPYKFEFNAETFTFHADICTLSEKQIKKQATLVELVHKPKAT 540
 Db 481 LVNRRPCFSALEVDYTPYKFEFNAETFTFHADICTLSEKQIKKQATLVELVHKPKAT 540

Qy 541 KEQLKAVMDDFAAFVEKCKKADDDKTCFAEKGKLVAAASQAALGL 585
 Db 541 KEQLKAVMDDFAAFVEKCKKADDDKTCFAEKGKLVAAASQAALGL 585

RESULT 7
 AAY83946
 ID AAY83946 standard; Protein; 585 AA.

XX AC AAY83946;
 XX DT 28-JUL-2000 (first entry)
 XX DE Yeast codon-biased recombinant human serum albumin protein.

XX KW Recombinant; human serum albumin; HSA; yeast codon bias; host cell;
 KW overlapping oligonucleotide; expression vector.

XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN CN1239103-A.
 XX PD 22-DEC-1999.
 XX PF 17-JUN-1998; 98CN-0102506.
 XX PR 17-JUN-1998; 98CN-0102506.
 XX PA (HAIJ-) HAIJI BIOENGINEERING CO LTD.
 XX PI Li S, Lu D;
 XX DR WPI; 2000-351198/31.
 XX DR N-PSDB; AAA10091.

PT Process for preparing recombinant human serum albumin - which comprises
 PT yeast biased sex codons
 XX Disclosure; Fig 1; 44pp; Chinese.

XX The method relates to a method of recombinantly producing human serum
 CC albumin (HSA) in yeast by altering the coding sequence of HSA to
 CC comprise a yeast codon bias. The complete HSA gene (AAA10091) was
 CC generated as three synthetic fragments (AAA10092-10094) joined by
 CC recombinant DNA technology. Each HSA fragment was synthesized from
 CC overlapping oligonucleotide fragments that were extended. This sequence
 CC represents the complete sequence of the HSA encoded by the human gene
 CC with a yeast codon bias. The invention also covers a recombinant
 CC expression vector, yeast host cells carrying the recombinant expression
 CC vector and the process for producing human serum albumin in the yeast
 CC host cell, especially in secretory mode.

XX Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 21; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1e-254;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHSEVAHREKDLGEENFKALVLIATAFYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 60
 Db 1 DAHSEVAHREKDLGEENFKALVLIATAFYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 60
 Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPRLVRPEV 120
 Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPRLVRPEV 120
 Qy 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
 Db 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
 Qy 181 KLDELDRDEGKASSAKQRLKASLOKFGRAFKAFAVARSORFPAEVSRLVTDLT 240

Db 181 KLDELDEGRASSAKQRLKCSLQKFCERAFKAWAVARLSQRPKAEVSKLVTDLTK 240
Qy 241 VHTTECHGDLLECCADRADLAKYICENQDSISSKLEKCECKPLLEKSHCIAEVENDEMPA 300
Db 241 VHTTECHGDLLECCADRADLAKYICENQDSISSKLEKCECKPLLEKSHCIAEVENDEMPA 300
Qy 301 DLPSLAADFVSKVCKNYAEAKDVFLGMPFLYEYARRHPDYSVVLLRLAKTYETTLK 360
Db 301 DLPSLAADFVSKVCKNYAEAKDVFLGMPFLYEYARRHPDYSVVLLRLAKTYETTLK 360
Qy 361 CAADPHCEYAKVDFEKPPLVEEPQNLKQNCSELFQGEYKFNQALLVRYTKVQVST 420
Db 361 CAADPHCEYAKVDFEKPPLVEEPQNLKQNCSELFQGEYKFNQALLVRYTKVQVST 420
Qy 421 PTLVEVSRLNGKVGSKCKKPEAKRMPCAEDYLSVNLQNLVLEKTPVSDRYTKCCTES 480
Db 421 PTLVEVSRLNGKVGSKCKKPEAKRMPCAEDYLSVNLQNLVLEKTPVSDRYTKCCTES 480
Qy 481 LVNRPCFSALEVDVTPKFEFNAETFTFHADICTLSEKERQIKKOTALVELVKHKPKAT 540
Db 481 LVNRPCFSALEVDVTPKFEFNAETFTFHADICTLSEKERQIKKOTALVELVKHKPKAT 540
Qy 541 KEQLKAVMDFFAAFEVKCKKADKCTCFABEGKKLVAASQAALGL 585
Db 541 KEQLKAVMDFFAAFEVKCKKADKCTCFABEGKKLVAASQAALGL 585

RESULT 8

ABB79006
ID ABB79006 standard; Protein: 585 AA.

AC ABB79006;

DT 01-AUG-2002 (first entry)

DE Human mature albumin protein SEQ ID NO:18.

Human; growth hormone; hGH; albumin; human serum albumin; HSA;
albumin fusion protein; cytostatic; anorectic; immunosuppressive;
antidiabetic; antirheumatic; antiarthritic; psoriatic; cancer;
non-Hodgkin's lymphoma; obesity; transplant rejection; psoriasis;
type I diabetes mellitus; rheumatoid arthritis.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Domain 1..194 /label= 1
FT Domain 1..105 /label= subdomain
FT Disulfide-bond 53..62
FT Disulfide-bond 75..91
FT Disulfide-bond 90..101
FT Region 106..119 /note= "flexible inter-subdomain linker region"
FT Domain 120..194 /label= subdomain
FT Disulfide-bond 124..169
FT Disulfide-bond 168..177
FT Domain 195..387 /label= 2
FT Domain 195..291 /label= subdomain
FT Disulfide-bond 245..253
FT Disulfide-bond 285..279
FT Disulfide-bond 278..289
FT Region 292..315 /note= "flexible inter-subdomain linker region"
FT Domain 316..387 /label= subdomain
FT Disulfide-bond 316..361
FT Disulfide-bond 360..369

FT Domain 388..585 /label= 3
FT Domain 388..491 /label= subdomain
FT Disulfide-bond 392..438
FT Disulfide-bond 437..448
FT Disulfide-bond 461..477
FT Disulfide-bond 476..487
FT Region 492..511 /note= "flexible inter-subdomain linker region"
FT Domain 512..585 /label= subdomain
FT Disulfide-bond 514..559
FT Disulfide-bond 558..567

XX WO200179442-A2.

XX 25-OCT-2001.

XX 12-APR-2001; 2001WO-US11850.

XX 12-APR-2000; 2000US-229358P.

PR 25-APR-2000; 2000US-199384P.

PR 21-DEC-2000; 2000US-256931P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Haseilte WA;

XX WPI; 2001-611723/70.

XX N-PSDB; ABN87288.

PT New albumin fusion proteins, useful for treating diseases and disorders
such as cancer, comprise therapeutic protein fused to albumin

PS Claim 1; Fig 11; 413pp; English.

XX The present invention describes an albumin fusion protein (I) comprising
a therapeutic protein: X and (a) fragment or variant of) albumin
comprising a the fully defined sequence in ABB79006 of 585 amino acids,
(where the fragment or variant has albumin or therapeutic protein: X
activity). (I) can have cytostatic, anorectic, immunosuppressive,
antidiabetic, antirheumatic, antiarthritic and psoriatic activities.
Albumin fusion proteins are stabilised therapeutic proteins e.g.
antibodies to C5, C242 and CD80 useful for treating various diseases
and disorders such as non-Hodgkin's lymphoma, cancer, obesity,
transplant rejection, type I diabetes mellitus, rheumatoid arthritis
and psoriasis. Fusing albumin to therapeutic proteins stabilises the
therapeutic protein, extends the shelf life and retains the in vitro or
in vivo biological activity. It also reduces the need to formulate
protein solutions with large excesses of carrier proteins to prevent
loss of therapeutic proteins due to factors such as binding to the
container. The fusion proteins are easily dispensed with a simple
formulation requiring minimal post storage manipulation. The fusion of
therapeutic proteins to albumin confers stability in aqueous or other
solution. The present sequence represents the mature human albumin (HA)
protein which is used in the exemplification of the present invention.

Qy Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 22; Length 585;
Best Local Similarity 100.0%; Pred. No. 1e-254;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFDLGEENFKALVLIATFAQYLOCCPEDHVKLVNTEFAKTCVADESAE 60
Db 1 DAHKSEVAHRFDLGEENFKALVLIATFAQYLOCCPEDHVKLVNTEFAKTCVADESAE 60
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
Qy 121 DVNCTAFHDNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180

Appendix

Db 121 DVMCTAFHDNEETFLKYLIEARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
Qy 181 KLDELDRSGKASSAKORLKCASLOKFGGFAKAWARLSORFPKAEFAEVSCLVDTLTK 240
Db 181 KLDELDRSGKASSAKORLKCASLOKFGGFAKAWARLSORFPKAEFAEVSCLVDTLTK 240
Qy 241 VHTCECHGDLLECADRADLAKYICENQDSISSKLEKCECEKPLLEKSHCIAEVENDEMPA 300
Db 241 VHTCECHGDLLECADRADLAKYICENQDSISSKLEKCECEKPLLEKSHCIAEVENDEMPA 300
Qy 301 DLPSLAADFVSKOVCKNYAEAKDVFLGMFLYFYARRHPDYSVLLLRLLAKTYETTLTK 360
Db 301 DLPSLAADFVSKOVCKNYAEAKDVFLGMFLYFYARRHPDYSVLLLRLLAKTYETTLTK 360
Qy 361 CAADPHCEYAKVDFEFLYEPONLJKONCELFQELGEYKFNALLVRYTKKVPQYST 420
Db 361 CAADPHCEYAKVDFEFLYEPONLJKONCELFQELGEYKFNALLVRYTKKVPQYST 420
Qy 421 PTLVEVSRNLKGVSKCKHPEAKMPCAEYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRNLKGVSKCKHPEAKMPCAEYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
Qy 481 LVNRRPCFSALEVDYTPVPEKFAETFTFHADICTLSEKQIKKQKOTALVELVKKHPRAT 540
Db 481 LVNRRPCFSALEVDYTPVPEKFAETFTFHADICTLSEKQIKKQKOTALVELVKKHPRAT 540
Qy 541 KQQLKAVMDDFAAFEKCKKADDKETCFABEGGKLVAAASQAALGL 585
Db 541 KQQLKAVMDDFAAFEKCKKADDKETCFABEGGKLVAAASQAALGL 585

RESULT 9

AAEL1399
ID AAEL1399 standard; Protein: 585 AA.

AC AAEL1399;
DT 12-FEB-2002 (first entry)
XX Human albumin (HA) protein.

XX Human; albumin; HA; fusion protein; immune system disorder; syphilis;
KW transplant rejection; blood related disorder; myocardial infarction;
KW hyperproliferative disorder; acute myeloid leukaemia; renal disorder;
KW glomerulonephritis; cardiovascular disorder; arrhythmia; rhinitis;
KW respiratory disorder; neurological disease; Alzheimer's disease;
KW endocrine disorder; pheochromocytoma; reproductive system disorder;
KW measles; gastrointestinal disorder; irritable bowel syndrome; HIV;
KW human immunodeficiency virus; wound healing; renal cell carcinoma;
KW melanoma; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 54..61
FT Domain /label= Loop_I
FT 76..89
FT Domain /label= Loop_II
FT 92..100
FT Domain /label= Loop_III
FT 170..176
FT Domain /label= Loop_IV
FT 247..252
FT Domain /label= Loop_V
FT 266..277
FT Domain /label= Loop_VI
FT 280..288
FT Domain /label= Loop_VII
FT 362..368
FT Domain /label= Loop_VIII
FT 439..447
FT Domain /label= Loop_IX

FT Domain 461..475
FT /label= Loop_x
FT Domain 478..486
FT /label= Loop_XI
FT Domain 560..566
FT /label= Loop_XII
XX WO200179258-A1.
XX 25-OCT-2001.
XX 12-APR-2001; 2001WO-US12008.
XX 12-APR-2000; 2000US-229358P.
XX 25-APR-2000; 2000US-199384P.
XX 21-DEC-2000; 2000US-256931P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (PRIN-) PRINCIPIA PHARM CORP.
XX Rosen CA, Sadeghi H, Prior CP, Turner AJ;
XX WPI; 2001-602931/68.
XX N-PSDB; AAD22287.
XX Albumin fusion proteins comprising a therapeutic protein and albumin,
XX useful in the treating metastatic renal cell carcinoma, metastatic
XX melanoma, malignant melanoma, renal cell carcinoma, HIV (human
XX immunodeficiency virus) or infection -
XX Claim 1; Fig 9; 325pp; English.

XX The invention relates to albumin fusion proteins comprising therapeutic
XX protein and human albumin (HA). The albumin fusion proteins are useful
XX in the treatment, prevention, diagnosis, and/or detection of diseases,
XX disorders such as immune system disorders (transplant rejection); blood
XX related disorders (myocardial infarction); hyperproliferative disorders
XX (childhood acute myeloid leukaemia); renal disorder (glomerulonephritis);
XX cardiovascular disorders (arrhythmias); respiratory disorders
XX (non-allergic rhinitis); neurological diseases (Alzheimer's disease);
XX endocrine disorders (pheochromocytoma); reproductive system disorders
XX (syphilis); infectious diseases (measles); gastrointestinal disorders
XX (irritable bowel syndrome) and wound healing. The albumin fusion
XX proteins are also used in the treatment of metastatic renal cell
XX carcinoma, metastatic melanoma, malignant melanoma and HIV (human
XX immunodeficiency virus) infection. Nucleic acid encoding albumin fusion
XX protein is useful in gene therapy. The present sequence is human
XX albumin (HA) protein.

SQ Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 22; Length 585;
Best Local Similarity 100.0%; Pred. No. le-254;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGGEENFKALVLIAFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 60
Db 1 DAHKSEVAHRFKDLGGEENFKALVLIAFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 60
Qy 61 NCDSLSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
Db 61 NCDSLSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
Qy 121 DVMCTAFHDNEETFLKYLIEARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
Db 121 DVMCTAFHDNEETFLKYLIEARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
Qy 181 KLDELDRSGKASSAKORLKCASLOKFGGFAKAWARLSORFPKAEFAEVSCLVDTLTK 240
Db 181 KLDELDRSGKASSAKORLKCASLOKFGGFAKAWARLSORFPKAEFAEVSCLVDTLTK 240
Qy 241 VHTCECHGDLLECADRADLAKYICENQDSISSKLEKCECEKPLLEKSHCIAEVENDEMPA 300
Db 241 VHTCECHGDLLECADRADLAKYICENQDSISSKLEKCECEKPLLEKSHCIAEVENDEMPA 300

Appended

Db 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
 QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYEVARRHPDYSVVLLRLAKTYETTTLEK 360
 Db 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYEVARRHPDYSVVLLRLAKTYETTTLEK 360
 QY 361 CAADPHCEYAKVDFEKPVEEPQNLKONCELFQOLGEYKFNALLVRYTKKVPQVST 420
 Db 361 CAADPHCEYAKVDFEKPVEEPQNLKONCELFQOLGEYKFNALLVRYTKKVPQVST 420
 QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
 Db 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
 QY 481 LVNRRPCFSALEVDVETVVPKEFNAETTFHADICTLSEKERQIKKQATLVLYVKKPKAT 540
 Db 481 LVNRRPCFSALEVDVETVVPKEFNAETTFHADICTLSEKERQIKKQATLVLYVKKPKAT 540
 QY 541 KEQLKAVMDDFAAFPVEKCCCKADKCTCFABEGKKLVAASQAALGL 585
 Db 541 KEQLKAVMDDFAAFPVEKCCCKADKCTCFABEGKKLVAASQAALGL 585

RESULT 10
 AAM52567
 ID AAM52567 standard; Protein; 585 AA.
 XX AC AAM52567;
 XX DT 05-FEB-2002 (first entry)
 XX DE Mature human serum albumin.
 XX KW Human; serum albumin; HA; antiinflammatory; immunosuppressive; cardiant;
 KW nootropic; neuroprotective; gene therapy; immune disorder; wound healing;
 KW hyperproliferative disorder; renal disorder; cardiovascular disorder;
 KW respiratory disorder; neurological disease; endocrine disorder;
 KW reproductive system disorder; infectious disease;
 KW gastrointestinal disorder.
 XX OS Homo sapiens.
 XX WO200179444-A2.
 XX PN 25-OCT-2001.
 XX PD 12-APR-2001; 2001WO-US12013.
 XX PR 12-APR-2000; 2000US-229358P.
 XX PR 25-APR-2000; 2000US-199384P.
 XX PR 21-DEC-2000; 2000US-256931P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX PA Rosen CA, Haseltine WA;
 XX PI WPI: 2001-616755/71.
 XX DR N-PSDB; ABA03057.
 XX XX
 PT Albumin fusion proteins comprising a therapeutic protein and albumin,
 PT useful in the treating immune system disorders (e.g. transplant
 PT rejection), blood related disorders (e.g. myocardial infarction) and
 PT hyperproliferative disorders -
 XX Claim 1; Fig 15; 606pp; English.
 XX PS
 CC The present invention relates to albumin fusion proteins, which comprise
 CC a therapeutic protein and albumin. The present sequence is the protein
 CC sequence for mature human serum albumin (HA), which was used to generate
 CC the fusion proteins of the present invention. The albumin fusion proteins
 CC are useful in the treatment, prevention, diagnosis, and/or detection of
 CC diseases/disorders such as immune system disorders (e.g. transplant
 CC rejection), blood related disorders (e.g. myocardial infarction),

CC hyperproliferative disorders (e.g. childhood acute myeloid leukemia),
 CC renal disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g.
 CC arrhythmias), respiratory disorders (e.g. non-allergic rhinitis),
 CC neurological diseases (e.g. Alzheimer's disease), endocrine disorders
 CC (e.g. pheochromocytoma), reproductive system disorders (e.g. syphilis),
 CC infectious diseases (e.g. measles), gastrointestinal disorders (e.g.
 CC irritable bowel syndrome) and wound healing.
 XX
 SQ Sequence 585 AA;
 Query Match 100.0%; Score 3103; DB 22; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1e-254;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHFRKDLGDFKALVLIAPAFYQLOCCPFEDHVKLVNEVTEFAKTCVADSAE 60
 Db 1 DAHSEVAHFRKDLGDFKALVLIAPAFYQLOCCPFEDHVKLVNEVTEFAKTCVADSAE 60
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFQHKDDNPNLRLVPEV 120
 Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFQHKDDNPNLRLVPEV 120
 QY 121 DVMTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
 Db 121 DVMTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
 QY 181 KLDELDEGKASSAKORLKCASLQKGFERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 240
 Db 181 KLDELDEGKASSAKORLKCASLQKGFERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 240
 QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
 Db 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
 QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYEVARRHPDYSVVLLRLAKTYETTTLEK 360
 Db 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYEVARRHPDYSVVLLRLAKTYETTTLEK 360
 QY 361 CAADPHCEYAKVDFEKPVEEPQNLKONCELFQOLGEYKFNALLVRYTKKVPQVST 420
 Db 361 CAADPHCEYAKVDFEKPVEEPQNLKONCELFQOLGEYKFNALLVRYTKKVPQVST 420
 QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
 Db 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
 QY 481 LVNRRPCFSALEVDVETVVPKEFNAETTFHADICTLSEKERQIKKQATLVLYVKKPKAT 540
 Db 481 LVNRRPCFSALEVDVETVVPKEFNAETTFHADICTLSEKERQIKKQATLVLYVKKPKAT 540
 QY 541 KEQLKAVMDDFAAFPVEKCCCKADKCTCFABEGKKLVAASQAALGL 585
 Db 541 KEQLKAVMDDFAAFPVEKCCCKADKCTCFABEGKKLVAASQAALGL 585

RESULT 11
 AAE13129
 ID AAE13129 standard; Protein; 585 AA.
 XX AC AAE13129;
 XX DT 28-JAN-2002 (first entry)
 XX DE Human albumin (HA).
 XX KW Human; albumin; HA; fusion protein; therapeutic protein; vulnary;
 KW immune system disorder; transplant rejection; blood related disorder;
 KW myocardial infarction; hyperproliferative disorder; glomerulonephritis;
 KW childhood acute myeloid leukemia; cardiovascular disorder; arrhythmia;
 KW respiratory disorder; gene therapy; non-allergic rhinitis; nootropic;
 KW neurological disease; Alzheimer's disease; reproductive system disorder;
 KW endocrine disorder; pheochromocytoma; infectious disease; antiarthritis;
 KW measles; gastrointestinal disorder; irritable bowel syndrome; syphilis;

wound healing; antiinflammatory; immunosuppressive; neuroprotective; cardiant; cytostatic; antileukaemic; antirheumatic; antimicrobial; renal disorder.
Homo sapiens.

Key Location/Qualifiers
Domain 54..61 /label= Loop_I
Domain 76..89 /label= Loop_II
Domain 92..100 /label= Loop_III
Domain 170..176 /label= Loop_IV
Domain 247..252 /label= Loop_V
Domain 266..277 /label= Loop_VI
Domain 280..288 /label= Loop_VII
Domain 362..368 /label= Loop_VIII
Domain 439..447 /label= Loop_IX
Domain 461..475 /label= Loop_X
Domain 478..486 /label= Loop_XI
Domain 560..566 /label= Loop_XII

WO200179443-A2.

25-OCT-2001.

12-APR-2001; 2001WO-US11924.

12-APR-2000; 2000US-229358P.

25-APR-2000; 2000US-199384P.

21-DEC-2000; 2000US-256931P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Haseltine WA;

WPI; 2001-616754/71.

N-PSDB; AAD21638.

Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction) and hyperproliferative disorders -

Claim 1; Fig 9; 380pp; English.

The invention relates to albumin fusion proteins comprising therapeutic protein and human albumin (HA). Therapeutic protein fused to albumin have an extended shelf-life. The albumin fusion proteins are useful in the treatment, prevention, diagnosis and/or detection of diseases, disorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction), hyperproliferative disorders (e.g. childhood acute myeloid leukaemia), renal disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmias), respiratory disorders (e.g. non-allergic rhinitis), neurological diseases (e.g. Alzheimer's disease), endocrine disorders (e.g. pheochromocytoma), reproductive system disorders (e.g. syphilis), infectious diseases (e.g. measles), gastrointestinal disorders (e.g. irritable bowel syndrome) and wound healing. Nucleic acids encoding albumin fusion protein is used in gene therapy. The present sequence is human albumin (HA) protein.

Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 22; Length 585;
Best Local Similarity 100.0%; Pred. No. 1e-254;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDGLGEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVADES 60
DB 1 DAHKSEVAHRFKDGLGEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVADES 60

QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLPLRVPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLPLRVPEV 120

QY 121 DVMTAFHDNEETFLKKYLYEIAARRHPYFYAPELFFAKRYKAAFTCCQAAADRAACLLP 180
DB 121 DVMTAFHDNEETFLKKYLYEIAARRHPYFYAPELFFAKRYKAAFTCCQAAADRAACLLP 180

QY 181 KLDELDRDEGKASSAKQRLKCSAQKQGERAFKAWAVARLSQRFPAEFAEYSKLVTDLTK 240
DB 181 KLDELDRDEGKASSAKQRLKCSAQKQGERAFKAWAVARLSQRFPAEFAEYSKLVTDLTK 240

QY 241 VHTCCCHGDLLECADRADLAKYICENODSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
DB 241 VHTCCCHGDLLECADRADLAKYICENODSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300

QY 301 DLPSLAADFVESKDVCKNYAEAKDVFGLMFLYEVARRHPDYVVLLRLRLAKTYETTTLEKC 360
DB 301 DLPSLAADFVESKDVCKNYAEAKDVFGLMFLYEVARRHPDYVVLLRLRLAKTYETTTLEKC 360

QY 361 CAADPHECYAKVDFEFPKPLVEEPQNLIKONCELFQOLGEYKFQNALLVRYTKKVPQVST 420
DB 361 CAADPHECYAKVDFEFPKPLVEEPQNLIKONCELFQOLGEYKFQNALLVRYTKKVPQVST 420

QY 421 PTLVEVSRNLGKVGSKCKKHPKAPCAEDYLSVNLQNLVLEHEKTPVSDRVTKCCTES 480
DB 421 PTLVEVSRNLGKVGSKCKKHPKAPCAEDYLSVNLQNLVLEHEKTPVSDRVTKCCTES 480

QY 481 LVNRRPCFSALEVDVETVPKPEFNAETFTFHADICTLSEKRIKKQTALVELVKHKPKAT 540
DB 481 LVNRRPCFSALEVDVETVPKPEFNAETFTFHADICTLSEKRIKKQTALVELVKHKPKAT 540

QY 541 KEQLKAYMDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585
DB 541 KEQLKAYMDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585

RESULT 12
AAE12403
ID AAE12403 standard; Protein; 585 AA.
AC AAE12403;
XX 18-DEC-2001 (first entry)
DT Human albumin (HA).
XX
DE
DE
XX
KW Human; albumin; HA; immune system disorder; transplant rejection;
KW blood related disorder; myocardial infarction; glomerulonephritis;
KW hyperproliferative disorder; childhood acute myeloid leukaemia;
KW renal cell carcinoma; cardiovascular disorder; vulnery; melanoma;
KW arhythmia; respiratory disorder; non-allergic rhinitis; antileukaemic;
KW neurological disease; Alzheimer's disease; endocrine disorder; measles;
KW pheochromocytoma; reproductive system disorder; neuroprotective; syphilis;
KW infectious disease; gastrointestinal disorder; wound healing; nyphtic;
KW irritable bowel syndrome; HIV; human immunodeficiency virus infection;
KW cytostatic; antiinflammatory; gene therapy; immunosuppressive; cardiant;
KW antiarthritic; antirheumatic; renal disorder; antimicrobial.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 54..61 /label= Loop_I
XX FT
XX FT

PS Claim 1; Fig 1; 20pp; English.

XX The invention related to a method for testing cancer cells. The method is
CC useful for measuring human cancer cell proliferation, particularly for
CC determining the potential for inhibiting cancer cells proliferation using
CC albumin-derived peptides. The invention is also useful for drug screening
CC assays, as well as for evaluating biopsied tumours. The present sequence
CC is human serum albumin (HSA) related to the invention.

XX Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 22; Length 585;
Best Local Similarity 100.0%; Pred. No. 1e-254;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHREKDLGEENFKALVLIATAFYAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 60
Db 1 DAHSEVAHREKDLGEENFKALVLIATAFYAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRPEV 120
QY 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAFTCCQAADKAACLLP 180
Db 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAFTCCQAADKAACLLP 180
QY 181 KLDELDEGKASSAKQRLKASLQKFGGERAFKAWAVARLSQRPFAEAEVSKLVTDLT 240
Db 181 KLDELDEGKASSAKQRLKASLQKFGGERAFKAWAVARLSQRPFAEAEVSKLVTDLT 240
QY 241 VHTTECHGDLLECADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
Db 241 VHTTECHGDLLECADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
QY 301 DLPSLAADFVSKDCKNYAEAKDVFLGMFLYEYARRHPDYSVLLLRLLAKTYETTLK 360
Db 301 DLPSLAADFVSKDCKNYAEAKDVFLGMFLYEYARRHPDYSVLLLRLLAKTYETTLK 360
QY 361 CAADPHCEYAKVDFEFLVEEONLJKONCELFQELGEYKFNALLVRYTKVPQVST 420
Db 361 CAADPHCEYAKVDFEFLVEEONLJKONCELFQELGEYKFNALLVRYTKVPQVST 420
QY 421 PTLVSVNLKGVSKCKHPEAKMPCAEYDLSVLNQLCVLHETKTPVSDRVTKCCYES 480
Db 421 PTLVSVNLKGVSKCKHPEAKMPCAEYDLSVLNQLCVLHETKTPVSDRVTKCCYES 480
QY 481 LVNRRPCFSALEVDYTPYKFEFNAETFTFHADICTLSEKERQIKKOTALVELVKKPKAT 540
Db 481 LVNRRPCFSALEVDYTPYKFEFNAETFTFHADICTLSEKERQIKKOTALVELVKKPKAT 540
QY 541 KEQLKAVMDDEFAAFVEKCKKADDETCFAEBGKLLVAASQAALGL 585
Db 541 KEQLKAVMDDEFAAFVEKCKKADDETCFAEBGKLLVAASQAALGL 585

RESULT 14

ID ABG63321 standard; protein; 585 AA.

XX AC ABG63321;

XX AC ABG63321;

XX DT 27-AUG-2002 (first entry)

XX Human serum albumin (HSA) protein.

XX Albumin fusion protein; therapeutic protein x; human albumin; HA;
KW human serum albumin; HSA; cancer; reproductive disorder;
KW digestive disorder; immune disorder; endocrine disorder;
KW haematopoietic disorder; neural disorder; connective disorder;
KW cytosolic; antifibrility; antinflammatory; antitumor;
KW immunomodulator; anti-HIV; antidiabetic; haemostatic; neurotropic;
KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;

KW osteopathic; antiarthritic.

OS Homo sapiens.

XX WO200177137-A1.

XX PD 18-OCT-2001.

XX PF 12-APR-2001; 2001WO-US11988.

XX PR 12-APR-2000; 2000US-229358P.

XX PR 25-APR-2000; 2000US-199384P.

XX PR 21-DEC-2000; 2000US-256931P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Haseltine WA;

XX DR WPI; 2002-010886/01.

XX DR N-PSDB; ABK93280.

XX PT New fusion protein for treating disease e.g. diabetes comprises an

XX PT albumin fused to a therapeutic protein -

XX PS Claim 1; Fig 15; 2102pp; English.

CC The present invention relates to albumin fusion proteins comprising a
CC therapeutic protein x and human albumin (HA), also known as human serum
CC albumin, HSA). The proteins are useful for treating a disease or
CC disorder that may be modulated by therapeutic protein x. The albumin
CC extends the shelf-life of protein x, and may increase its biological
CC in vitro/in vivo activity. The protein is useful for treating and
CC diagnosing disorders such as cancer, reproductive disorders, digestive
CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders
CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders
CC (e.g. diabetes), haematopoietic disorders, neural disorders
CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,
CC encephalomyelitis, meningitis, schizophrenia), and connective disorders
CC (e.g. osteoporosis, arthritis). The present sequence represents HSA
CC (HA) protein.

XX SQ Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 23; Length 585;
Best Local Similarity 100.0%; Pred. No. 1e-254;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHREKDLGEENFKALVLIATAFYAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 60
Db 1 DAHSEVAHREKDLGEENFKALVLIATAFYAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRPEV 120
QY 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAFTCCQAADKAACLLP 180
Db 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAFTCCQAADKAACLLP 180
QY 181 KLDELDEGKASSAKQRLKASLQKFGGERAFKAWAVARLSQRPFAEAEVSKLVTDLT 240
Db 181 KLDELDEGKASSAKQRLKASLQKFGGERAFKAWAVARLSQRPFAEAEVSKLVTDLT 240
QY 241 VHTTECHGDLLECADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
Db 241 VHTTECHGDLLECADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
QY 301 DLPSLAADFVSKDCKNYAEAKDVFLGMFLYEYARRHPDYSVLLLRLLAKTYETTLK 360
Db 301 DLPSLAADFVSKDCKNYAEAKDVFLGMFLYEYARRHPDYSVLLLRLLAKTYETTLK 360
QY 361 CAADPHCEYAKVDFEFLVEEONLJKONCELFQELGEYKFNALLVRYTKVPQVST 420
Db 361 CAADPHCEYAKVDFEFLVEEONLJKONCELFQELGEYKFNALLVRYTKVPQVST 420

Db 361 CAADPHCYAKVDFEKPVLVEEPQNLKQNCLEFQOLGKYKFNALLVRYTKVPQVST 420
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVHEKTPVSDRYTKCCTES 480
Db 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVHEKTPVSDRYTKCCTES 480
QY 481 LVNRRPCFSALEVDETVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
Db 481 LVNRRPCFSALEVDETVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
QY 541 KEOLKAVMDDFAAFVEKCKKADDDKTCFAEEGKGLVAASQAALGL 585
Db 541 KEOLKAVMDDFAAFVEKCKKADDDKTCFAEEGKGLVAASQAALGL 585

RESULT 15
ABJ00986
ID ABJ00986 standard; Protein; 585 AA.
AC ABJ00986;
XX
XX
DT 05-SEP-2002 (first entry)
XX
DE B lymphocyte stimulator protein binding peptide related protein.
XX
KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Homo sapiens.
XX
PN WO200216411-A2.
XX
XX 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US25850.
XX
XX 18-AUG-2000; 2000US-226700P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
PI
XX WPI; 2002-499775/53.
DR
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B Lymphocyte stimulator binding polypeptide -
PT
XX Disclosure; Page 379-382; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a protein described
CC in the invention.
XX
SQ Sequence 585 AA;

Best Local Similarity 100.0%; Pred. No. 1e-254;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHFRKDLGGENFKALVLIAPAOYLQCCPPEDHVKLVNEVTEFAKTCVADESAAE 60
Db 1 DAHSEVAHFRKDLGGENFKALVLIAPAOYLQCCPPEDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVPEV 120
QY 121 DVNCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTBCCQAADKAACLLP 180
Db 121 DVNCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTBCCQAADKAACLLP 180
QY 181 KLDELDEGKASSAKORLKCASLOKFGERAFKAWARLSORPKAFBAFVSKLYTDLTK 240
Db 181 KLDELDEGKASSAKORLKCASLOKFGERAFKAWARLSORPKAFBAFVSKLYTDLTK 240
QY 241 VHTCCCHGDLLECCADDDRADLAKYICENQDSISSKLECCCKPILLEKSHCIAEVENDEMPA 300
Db 241 VHTCCCHGDLLECCADDDRADLAKYICENQDSISSKLECCCKPILLEKSHCIAEVENDEMPA 300
QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVVLRLRLAKTYETTLEKC 360
Db 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVVLRLRLAKTYETTLEKC 360
QY 361 CAADPHCYAKVDFEKPVLVEEPQNLKQNCLEFQOLGKYKFNALLVRYTKVPQVST 420
Db 361 CAADPHCYAKVDFEKPVLVEEPQNLKQNCLEFQOLGKYKFNALLVRYTKVPQVST 420
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVHEKTPVSDRYTKCCTES 480
Db 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVHEKTPVSDRYTKCCTES 480
QY 481 LVNRRPCFSALEVDETVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
Db 481 LVNRRPCFSALEVDETVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
QY 541 KEOLKAVMDDFAAFVEKCKKADDDKTCFAEEGKGLVAASQAALGL 585
Db 541 KEOLKAVMDDFAAFVEKCKKADDDKTCFAEEGKGLVAASQAALGL 585

Search completed: April 24, 2003, 07:25:22
Job time : 81 secs